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(54) Title: MODIFIED HIV ENV POLYPEPTIDES

#### (57) Abstract

Polynucleotide encoding modified HIV Env polypeptides are disclosed. The Env polypeptides are modified so as to expose at least part of the CD4 binding region. Methods of diagnosis, treatment and prevention using the polynucleotides and polypeptides are also provided.

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#### MODIFIED HIV ENV POLYPEPTIDES

## Technical Field

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The invention relates generally to modified HIV envelope (Env) polypeptides which are useful as immunizing agents or for generating an immune response in a subject, for example a cellular immune response or a protective immune response. More particularly, the invention relates Env polypeptides such as gp120, gp140 or gp160, wherein at least one of the native  $\beta$ -sheet configurations has been modified. The invention also pertains to methods of using these polypeptides to elicit an immune response against a broad range of HIV subtypes.

#### Background of the Invention

The human immunodeficiency virus (HIV-1, also referred to as HTLV-III, LAV or HTLV-III/LAV) is the etiological agent of the acquired immune deficiency syndrome (AIDS) and related disorders. (see, e.g., Barre-Sinoussi, et al., (1983) Science 220:868-871; Gallo et al. (1984) Science 224:500-503; Levy et al., (1984) Science 225:840-842; Siegal et al., (1981) N. Engl. J. Med. 305:1439-1444). AIDS patients usually have a long asymptomatic period followed by the progressive degeneration of the immune system and the central nervous system. Replication of the virus is highly regulated, and both latent and lytic infection of the CD4 positive helper subset of T-lymphocytes occur in tissue culture (Zagury et al., (1986) Science 231:850-853). Molecular studies of HIV-1 show that it encodes a number of genes (Ratner et al., (1985) Nature 313:277-284; Sanchez-Pescador et al., (1985) Science 227:484-492), including three structural genes -- gag, pol and env -- that are common to all retroviruses. Nucleotide sequences from viral genomes of other retroviruses, particularly HIV-2 and simian immunodeficiency viruses, SIV (previously referred to as STLV-III), also contain these structural genes. (Guyader et al., (1987) Nature 326:662-669; Chakrabarti et al., (1987) Nature

The envelope protein of HIV-1, HIV-2 and SIV is a glycoprotein of about 160 kd (gp160). During virus infection of the host cell, gp160 is cleaved by host cell proteases to form gp120 and the integral membrane protein, gp41. The gp41 portion is anchored in the

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membrane bilayer of virion, while the gp120 segment protrudes into the surrounding environment. gp120 and gp41 are more covalently associated and free gp120 can be released from the surface of virions and infected cells.

As depicted in Figure 1, crystallography studies of the gp120 core polypeptide indicate that this polypeptide is folded into two major domains having certain emanating structures. The inner domain (inner with respect to the N and C terminus) features a two-helix, two-stranded bundle with a small five-stranded  $\beta$ -sandwich at its termini-proximal end and a projection at the distal end from which the V1/V2 stem emanates. The outer domain is a staked double barrel that lies along side the inner domain so that the outer barrel and inner bundle axes are approximately parallel. Between the distal inner domain and the distal outer domain is a four-stranded bridging sheet which holds a peculiar minidomain in contact with, but distinct from, the inner, the outer domain, and the V1/V2 domain. The bridging sheet is composed of four  $\beta$ -strand structures ( $\beta$ -3,  $\beta$ -2,  $\beta$ -21,  $\beta$ -20, shown in Figure 1). The bridging region can be seen in Figure 1 packing primarily over the inner domain, although some surface residues of the outer domain, such as Phe 382, reach into the bridging sheet to form part of its hydrophobic core.

The basic unit of the  $\beta$ -sheet conformation of the bridging sheet region is the  $\beta$ -strand which exists as a less tightly coiled helix, with 2.0 residues per turn. The  $\beta$ -strand conformation is only stable when incorporated into a  $\beta$ -sheet, where hydrogen bonds with close to optimal geometry are formed between the peptide groups on adjacent  $\beta$ -strands; the dipole moments of the strands are also aligned favorably. Side chains from adjacent residues of the same strand protrude from opposite sides of the sheet and do not interact with each other, but have significant interactions with their backbone and with the side chains of neighboring strands. For a general description of  $\beta$ -sheets, see, e.g., T.E. Creighton, Proteins: Structures and Molecular Properties (W.H. Freeman and Company, 1993); and A.L. Lehninger, Biochemistry (Worth Publishers, Inc., 1975).

The gp120 polypeptide is instrumental in mediating entry into the host cell. Recent studies have indicated that binding of CD4 to gp120 induces a conformational change in Env that allows for binding to a co-receptor (e.g., a chemokine receptor) and subsequent entry of the virus into the cell. (Wyatt, R., et al. (1998) Nature 393:705-711; Kwong, P., et al. (1998) Nature 393:648-659). Referring again to Figure 1, CD4 is bound into a depression formed at the interface of the outer domain, the inner domain and the bridging sheet of gp120.

Immunogenicity of the gp120 polypeptide has also been studied. For example, individuals infected by HIV-1 usually develop antibodies that can neutralize the virus in *in vitro* assays, and this response is directed primarily against linear neutralizing determinants in the third variable loop of gp120 glycoprotein (Javaherian, K., et al. (1989) *Proc. Natl. Acad. Sci.* 86:6786-6772; Matsushita, M., et al. (1988) *J. Virol.* 62:2107-2144; Putney, S., et al. (1986) *Science* 234:1392-1395; Rushe, J. R., et al. (1988) *Proc. Nat. Acad. Sci. USA* 85: 3198-3202.). However, these antibodies generally exhibit the ability to neutralize only a limited number of HIV-1 strains (Matthews, T. (1986) *Proc. Natl. Acad. Sci. USA*. 83:9709-9713; Nara, P. L., et al. (1988) *J. Virol.* 62:2622-2628; Palker, T. J., et al. (1988) *Proc. Natl. Acad. Sci. USA*. 85:1932-1936). Later in the course of HIV infection in humans, antibodies capable of neutralizing a wider range of HIV-1 isolates appear (Barre-Sinoussi, F., et al. (1983) *Science* 220:868-871; Robert-Guroff, M., et al. (1985) *Nature* (London) 316:72-74; Weis, R., et al. (1985) *Nature* (London) 316:72-74; Weis, R., et al. (1985) *Nature* (London)

Recent work done by Stamatatos et al (1998) AIDS Res Hum Retroviruses

14(13):1129-39, shows that a deletion of the variable region 2 from a HIV-1<sub>SF162</sub> virus, which utilizes the CCR-5 co-receptor for virus entry, rendered the virus highly susceptible to serum-mediated neutralization. This V2 deleted virus was also neutralized by sera obtained from patients infected not only with clade B HIV-1 isolates but also with clade A, C, D and F HIV-1 isolates. However, deletion of the variable region 1 had no effect. Deletion of the variable regions 1 and 2 from a LAI isolate HIV-I<sub>IIIB</sub> also increased the susceptibility to neutralization by monoclonal antibodies whose epitopes are located within the V3 loop, the CD4-binding site, and conserved gp120 regions (Wyatt, R., et al. (1995) J Virol. 69:5723-5733). Rabbit immunogenicity studies done with the HIV-1 virus with deletions in the V1/V2 and V3 region from the LAI strain, which uses the CXCR4 co-receptor for virus entry, showed no improvement in the ability of Env to raise neutralizing antibodies (Leu et al. (1998) AIDS Res. and Human Retroviruses. 14:151-155).

Further, a subset of the broadly reactive antibodies, found in most infected individuals, interferes with the binding of gp120 and CD4 (Kang, C.-Y., et al. (1991) *Proc. Natl. Acad. Sci. USA.* 88:6171-6175; McDougal, J. S., et al. (1986) *J. Immunol.* 137:2937-2944). Other antibodies are believed to bind to the chemokine receptor binding region after CD4 has bound to Env (Thali et al. (1993) *J. Virol.* 67:3978-3988). The fact that neutralizing

antibodies generated during the course of HIV infection do not provide permanent antiviral effect may in part be due to the generation of "neutralization escapes" virus mutants and to the general decline in the host immune system associated with pathogenesis. In contrast, the presence of pre-existing neutralizing antibodies upon initial HIV-1 exposure will likely have a protective effect.

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It is widely thought that a successful vaccine should be able to induce a strong, broadly neutralizing antibody response against diverse HIV-1 strains (Montefiori and Evans (1999) AIDS Res. Hum. Ret. 15(8):689-698; Bolognesi, D.,P., et al. (1994) Ann. Int. Med. 8:603-611; Haynes, B., F., et al. (1996) Science; 271: 324-328.). Neutralizing antibodies, by attaching to the incoming virions, can reduce or even prevent their infectivity for target cells and prevent the cell-to-cell spread of virus in tissue culture (Hu et al. (1992) Science 255:456-459; Burton, D.,R. and Montefiori, D. (1997) AIDS 11(suppl. A): 587-598). However as described above, antibodies directed against gp120 do not generally exhibit broad antibody responses against different HIV strains.

Currently, the focus of vaccine development, from the perspective of humoral immunity, is on the neutralization of primary isolates that utilize the CCR5 chemokine coreceptor believed to be important in virus entry (Zhu, T., et al. (1993) Science 261:1179-1181; Fiore, J., et al. (1994) Virology; 204:297-303). These viruses are generally much more resistant to antibody neutralization than T-cell line adapted strains that use the CXCR4 coreceptor, although both can be neutralized in vitro by certain broadly and potent acting monoclonal antibodies, such as IgG1b12, 2G12 and 2F5 (Trkola, A., et al. (1995) J. Virol. 69:6609-6617; D'Sousa PM., et al (1997) J. Infect. Dis. 175:1062-1075). These monoclonal antibodies are directed to the CD4 binding site, a glycosylation site and to the gp41 fusion domain, respectively. The problem that remains, however, is that it is not known how to induce antibodies of the appropriate specificity by vaccination. Antibodies (Abs) elicited by gp120 glycoprotein from a given isolate are usually only able to neutralize closely related viruses generally from similar, usually from the same, HIV-1 subtype.

Despite the above approaches, there remains a need for Env antigens that can elicit an immunological response (e.g., neutralizing and/or protective antibodies) in a subject against multiple HIV strains and subtypes, for example when administered as a vaccine. The present invention solves these and other problems by providing modified Env polypeptides (e.g., gp120) to expose epitopes in or near the CD4 binding site.

## Summary of the Invention

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In accordance with the present invention, modified HIV Env polypeptides are provided. In particular, deletions and/or mutations are made in one or more of the 4- $\beta$  antiparallel-bridging sheet in the HIV Env polypeptide. In this way, enough structure is left to allow correct folding of the polypeptide, for example of gp120, yet enough of the bridging sheet is removed to expose the CD4 groove, allowing an immune response to be generated against epitopes in or near the CD4 binding site of the Env polypeptide (e.g., gp120).

In one aspect, the invention includes a polynucleotide encoding a modified HIV Env polypeptide wherein the polypeptide has at least one modified (e.g., deleted or replaced) amino acid residue deleted in the region corresponding to residues 421 to 436 relative to HXB-2, for example the constructs depicted in Figures 6-29 (SEQ ID NOs:3 to 26). In certain embodiments, the polynucleotide also has the region corresponding to residues 124-198 of the polypeptide HXB-2 (e.g., V1/V2) deleted and at least one amino acid deleted or replaced in the regions corresponding to the residues 119 to 123 and 199 to 210, relative to HXB-2. In other embodiments, these polynucleotides encode Env polypeptides having at least one amino acid of the small loop of the bridging sheet (e.g., amino acid residues 427 to 429 relative to HXB-2) deleted or replaced. The amino acid sequences of the modified polypeptides encoded by the polynucleotides of the present invention can be based on any HIV variant, for example SF162.

In another aspect, the invention includes immunogenic modified HIV Env polypeptides having at least one modified (e.g., deleted or replaced) amino acid residue deleted in the region corresponding to residues 421 to 436 relative to HXB-2, for example a deletion or replacement of one amino acids in the small loop region (e.g., amino acid residues 427 to 429 relative to HXB-2). These polypeptides may have modifications (e.g., a deletion or a replacement) of at least one amino acid between about amino acid residue 420 and amino acid residue 436, relative to HXB-2 and, optionally, may have deletions or truncations of the V1 and/or V2 regions. The immunogenic, modified polypeptides of the present invention can be based on any HIV variant, for example SF162.

In another aspect, the invention includes a vaccine composition comprising any of the polynucleotides encoding modified Env polypeptides described above. Vaccine compositions comprising the modified Env polypeptides and, optionally, an adjuvant are also included in the invention.

In yet another aspect, the invention includes a method of inducing an immune response in subject comprising, administering one or more of the polynucleotides or constructs described above in an amount sufficient to induce an immune response in the subject. In certain embodiments, the method further comprises administering an adjuvant to the subject.

In another aspect, the invention includes a method of inducing an immune response in a subject comprising administering a composition comprising any of the modified Env polypeptides described above and an adjuvant. The composition is administered in an amount sufficient to induce an immune response in the subject.

In another aspect, the invention includes a method of inducing an immune response in a subject comprising

- (a) administering a first composition comprising any of the polynucleotides described above in a priming step and
- (b) administering a second composition comprising any of the modified Env polypeptides described above, as a booster, in an amount sufficient to induce an immune response in the subject. In certain embodiments, the first composition, the second composition or both the first and second compositions further comprise an adjuvant.

These and other embodiments of the subject invention will readily occur to those of skill in the art in light of the disclosure herein.

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#### Brief Description of the Drawings

Figure 1 is a schematic depiction of the tertiary structure of the HIV-1<sub>HXB-2</sub> Env gp120 polypeptide, as determined by crystallography studies.

Figures 2A-C depict alignment of the amino acid sequence of wild-type HIV-1<sub>HXB-2</sub> Env gp160 polypeptide (SEQ ID NO:1) with amino acid sequence of HIV variants SF162 (shown as "162") (SEQ ID NO:2), SF2, CM236 and US4. Arrows indicate the regions that are deleted or replaced in the modified polypeptides. Black dots indicate conserved cysteine residues. The star indicates the position of the last amino acid in gp120.

Figures 3A-J depict alignment of nucleotide sequences of polynucleotides encoding modified Env polypeptides having V1/V2 deletions. The unmodified amino acid residues encoded by these sequences correspond to wildtype SF162 residues but are numbered relative to HXB-2.

Figures 4A-M depict alignment of nucleotide sequences of polynucleotides encoding modified Env polypeptides having deletions or replacements in the small loop. The unmodified amino acid residues encoded by these sequences correspond to wildtype SF162 residues but are numbered relative to HXB-2.

Figures 5A-N depict alignment of nucleotide sequences of polynucleotides encoding modified Env polypeptides having both V1/V2 deletions and, in addition, deletions or replacements in the small loop. The unmodified amino acid residues encoded by these sequences correspond to wildtype SF162 residues but are numbered relative to HXB-2.

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Figure 6 depicts the nucleotide sequence of the construct designated Val120-Ala204 (SEQ ID NO:3).

Figure 7 depicts the nucleotide sequence of the construct designated Val120-Ile201 (SEQ ID NO:4).

Figure 8 depicts the nucleotide sequence of the construct designated Val120-Ile201B (SEQ ID NO:5).

Figure 9 depicts the nucleotide sequence of the construct designated Lys121-Val200 (SEQ ID NO:6).

Figure 10 depicts the nucleotide sequence of the construct designated Leu122-Ser199 (SEQ ID NO:7).

Figure 11 depicts the nucleotide sequence of the construct designated Val120-Thr202 (SEQ ID NO:8).

Figure 12 depicts the nucleotide sequence of the construct designated Trp427-Gly431 (SEQ ID NO:9).

Figure 13 depicts the nucleotide sequence of the construct designated Arg426-Gly431 (SEQ ID NO:10).

Figure 14 depicts the nucleotide sequence of the construct designated Arg426-Gly431B (SEQ ID NO:11).

Figure 15 depicts the nucleotide sequence of the construct designated Arg426-Lys432 (SEQ ID NO:12).

Figure 16 depicts the nucleotide sequence of the construct designated Asn425-Lys432 (SEQ ID NO:13).

Figure 17 depicts the nucleotide sequence of the construct designated Ile424-Ala433 (SEQ ID NO:14).

Figure 18 depicts the nucleotide sequence of the construct designated Ile423-Met434 (SEQ ID NO:15).

Figure 19 depicts the nucleotide sequence of the construct designated Gln422-Tyr435 (SEQ ID NO:16).

Figure 20 depicts the nucleotide sequence of the construct designated Gln422-Tyr435B (SEQ ID NO:17).

Figure 21 depicts the nucleotide sequence of the construct designated Leu122-Ser199;Arg426-Gly431 (SEQ ID NO:18).

Figure 22 depicts the nucleotide sequence of the construct designated Leu122-Ser199;Arg426-Lys432 (SEQ ID NO:19).

Figure 23 depicts the nucleotide sequence of the construct designated Leu122-Ser199; Trp427-Gly431 (SEQ ID NO:20).

Figure 24 depicts the nucleotide sequence of the construct designated Lys121-Val200; Asn425-Lys432 (SEQ ID NO:21).

Figure 25 depicts the nucleotide sequence of the construct designated Val120-Ile201; Ile424-Ala433 (SEQ ID NO:22).

Figure 26 depicts the nucleotide sequence of the construct designated Val120-Ile201B; Ile424-Ala433 (SEQ ID NO:23).

Figure 27 depicts the nucleotide sequence of the construct designated Val120-Thr202; Ile424-Ala433 (SEQ ID NO:24).

Figure 28 depicts the nucleotide sequence of the construct designated Val127-Asn195 (SEQ ID NO:25).

Figure 29 depicts the nucleotide sequence of the construct designated Val127-Asn195; Arg426-Gly431 (SEQ ID NO:26).

# Detailed Description of the Invention

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The practice of the present invention will employ, unless otherwise indicated, conventional methods of protein chemistry, viral immunobiology, molecular biology and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., T.E. Creighton, <u>Proteins: Structures and Molecular Properties</u> (W.H. Freeman and Company, 1993); Nelson L.M. and Jerome H.K. <u>HIV Protocols in</u> Methods in Molecular Medicine, vol. 17, 1999; Sambrook, et al., <u>Molecular Cloning: A</u>

<u>Laboratory Manual</u> (Cold Spring Harbor Laboratory, 1989); F.M. Ausubel et al. <u>Current Protocols in Molecular Biology</u>, Greene Publishing Associates & Wiley Interscience New York; and Lipkowitz and Boyd, <u>Reviews in Computational Chemistry</u>, volumes 1-present (Wiley-VCH, New York, New York, 1999).

It must be noted that, as used in this specification and the appended claims, the singular forms "a", "an" and "the" include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "a polypeptide" includes a mixture of two or more polypeptides, and the like.

#### **Definitions**

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In describing the present invention, the following terms will be employed, and are intended to be defined as indicated below.

The terms "polypeptide," and "protein" are used interchangeably herein to denote any polymer of amino acid residues. The terms encompass peptides, oligopeptides, dimers, multimers, and the like. Such polypeptides can be derived from natural sources or can be synthesized or recombinantly produced. The terms also include postexpression modifications of the polypeptide, for example, glycosylation, acetylation, phosphorylation, etc.

A polypeptide as defined herein is generally made up of the 20 natural amino acids Ala (A), Arg (R), Asn (N), Asp (D), Cys (C), Gln (Q), Glu (E), Gly (G), His (H), Ile (I), Leu (L), Lys (K), Met (M), Phe (F), Pro (P), Ser (S), Thr (T), Trp (W), Tyr (Y) and Val (V) and may also include any of the several known amino acid analogs, both naturally occurring and synthesized analogs, such as but not limited to homoisoleucine, asaleucine, 2-(methylenecyclopropyl)glycine, S-methylcysteine, S-(prop-l-enyl)cysteine, homoserine, ornithine, norleucine, norvaline, homoarginine, 3-(3-carboxyphenyl)alanine, cyclohexylalanine, mimosine, pipecolic acid, 4-methylglutamic acid, canavanine, 2,3-diaminopropionic acid, and the like. Further examples of polypeptide agents which will find use in the present invention are set forth below.

By "geometry" or "tertiary structure" of a polypeptide or protein is meant the overall 3-D configuration of the protein. As described herein, the geometry can be determined, for example, by crystallography studies or by using various programs or algorithms which predict the geometry based on interactions between the amino acids making up the primary and secondary structures.

By "wild type" polypeptide, polypeptide agent or polypeptide drug, is meant a naturally occurring polypeptide sequence, and its corresponding secondary structure. An "isolated" or "purified" protein or polypeptide is a protein which is separate and discrete from a whole organism with which the protein is normally associated in nature. It is apparent that the term denotes proteins of various levels of purity. Typically, a composition containing a purified protein will be one in which at least about 35%, preferably at least about 40-50%, more preferably, at least about 75-85%, and most preferably at least about 90% or more, of the total protein in the composition will be the protein in question.

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By "Env polypeptide" is meant a molecule derived from an envelope protein, preferably from HIV Env. The envelope protein of HIV-1 is a glycoprotein of about 160 kd (gp160). During virus infection of the host cell, gp160 is cleaved by host cell proteases to form gp120 and the integral membrane protein, gp41. The gp41 portion is anchored in (and spans) the membrane bilayer of virion, while the gp120 segment protrudes into the surrounding environment. As there is no covalent attachment between gp120 and gp41, free gp120 is released from the surface of virions and infected cells. Env polypeptides may also include gp140 polypeptides. Env polypeptides can exist as monomers, dimers or multimers.

By a "gp120 polypeptide" is meant a molecule derived from a gp120 region of the Env polypeptide. Preferably, the gp120 polypeptide is derived from HIV Env. The primary amino acid sequence of gp120 is approximately 511 amino acids, with a polypeptide core of about 60,000 daltons. The polypeptide is extensively modified by N-linked glycosylation to increase the apparent molecular weight of the molecule to 120,000 daltons. The amino acid sequence of gp120 contains five relatively conserved domains interspersed with five hypervariable domains. The positions of the 18 cysteine residues in the gp120 primary sequence of the HIV-1<sub>HXB-2</sub> (hereinafter "HXB-2") strain, and the positions of 13 of the approximately 24 N-linked glycosylation sites in the gp120 sequence are common to most, if not all, gp120 sequences. The hypervariable domains contain extensive amino acid substitutions, insertions and deletions. Despite this variation, most, if not all, gp120 sequences preserve the virus's ability to bind to the viral receptor CD4. A "gp120 polypeptide" includes both single subunits or multimers.

Env polypeptides (e.g., gp120, gp140 and gp160) include a "bridging sheet" comprised of 4 anti-parallel  $\beta$ -strands ( $\beta$ -2,  $\beta$ -3,  $\beta$ -20 and  $\beta$ -21) that form a  $\beta$ -sheet. Extruding from one pair of the  $\beta$ -strands ( $\beta$ -2 and  $\beta$ -3) are two loops, V1 and V2. The  $\beta$ -2

sheet occurs at approximately amino acid residue 119 (Cys) to amino acid residue 123 (Thr) while β-3 occurs at approximately amino acid residue 199 (Ser) to amino acid residue 201 (Ile), relative to HXB-2. The "V1/V2 region" occurs at approximately amino acid positions 126 (Cys) to residue 196 (Cys), relative to HXB-2. (see, e.g., Wyatt et al. (1995) *J. Virol.* 69:5723-5733; Stamatatos et al. (1998) *J. Virol.* 72:7840-7845). Extruding from the second pair of β-strands (β-20 and β-21) is a "small-loop" structure, also referred to herein as "the bridging sheet small loop." In HXB-2, β-20 extends from about amino acid residue 422 (Gln) to amino acid residue 426 (Met) while β-21 extends from about amino acid residue 430 (Val) to amino acid residue 435 (Tyr). In variant SF162, the Met-426 is an Arg (R) residue. The "small loop" extends from about amino acid residue 427 (Trp) through 429 (Lys), relative to HXB-2. A representative diagram of gp120 showing the bridging sheet, the small loop, and V1/V2 is shown in Figure 1. In addition, alignment of the amino acid sequences of Env polypeptide gp160 of selected variants is shown, relative to HXB-2, in Figures 2A-C.

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Furthermore, an "Env polypeptide" or "gp120 polypeptide" as defined herein is not limited to a polypeptide having the exact sequence described herein. Indeed, the HIV genome is in a state of constant flux and contains several variable domains which exhibit relatively high degrees of variability between isolates. It is readily apparent that the terms encompass Env (e.g., gp120) polypeptides from any of the identified HIV isolates, as well as newly identified isolates, and subtypes of these isolates. Descriptions of structural features are given herein with reference to HXB-2. One of ordinary skill in the art in view of the teachings of the present disclosure and the art can determine corresponding regions in other HIV variants (e.g., isolates HIV<sub>IIIb</sub>, HIV<sub>SF2</sub>, HIV-1<sub>SF162</sub>, HIV-1<sub>SF170</sub>, HIV<sub>LAV</sub>, HIV<sub>LAI</sub>, HIV<sub>MN</sub>, HIV-1<sub>CM235</sub>,, HIV-1<sub>US4</sub>, other HIV-1 strains from diverse subtypes(e.g., subtypes, A through G, and O), HIV-2 strains and diverse subtypes (e.g., HIV-2<sub>UC1</sub> and HIV-2<sub>UC2</sub>), and simian immunodeficiency virus (SIV). (See, e.g., Virology, 3rd Edition (W.K. Joklik ed. 1988); Fundamental Virology, 2nd Edition (B.N. Fields and D.M. Knipe, eds. 1991); Virology, 3rd Edition (Fields, BN, DM Knipe, PM Howley, Editors, 1996, Lippincott-Raven, Philadelphia, PA; for a description of these and other related viruses), using for example, sequence comparison programs (e.g., BLAST and others described herein) or identification and alignment of structural features (e.g., a program such as the "ALB" program described herein that can identify  $\beta$ -sheet regions). The actual amino acid sequences of the modified Env polypeptides can be based on any HIV variant.

Additionally, the term "Env polypeptide" (e.g., "gp120 polypeptide") encompasses proteins which include additional modifications to the native sequence, such as additional internal deletions, additions and substitutions. These modifications may be deliberate, as through site-directed mutagenesis, or may be accidental, such as through naturally occurring mutational events. Thus, for example, if the Env polypeptide is to be used in vaccine compositions, the modifications must be such that immunological activity (i.e., the ability to elicit an antibody response to the polypeptide) is not lost. Similarly, if the polypeptides are to be used for diagnostic purposes, such capability must be retained.

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Thus, a "modified Env polypeptide" is an Env polypeptide (e.g., gp120 as defined above), which has been manipulated to delete or replace all or a part of the bridging sheet portion and, optionally, the variable regions V1 and V2. Generally, modified Env (e.g., gp120) polypeptides have enough of the bridging sheet removed to expose the CD4 binding site, but leave enough of the structure to allow correct folding (e.g., correct geometry). Thus, modifications to the  $\beta$ -20 and  $\beta$ -21 regions (between about amino acid residues 420 and 435 relative to HXB-2) are preferred. Additionally, modifications to the  $\beta$ -2 and  $\beta$ -3 regions (between about amino acid residues 119 (Cys) and 201 (Ile)) and modifications (e.g., truncations) to the V1 and V2 loop regions may also be made. Although not all possible  $\beta$ -sheet and V1/V2 modifications have been exemplified herein, it is to be understood that other disrupting modifications are also encompassed by the present invention.

Normally, such a modified polypeptide is capable of secretion into growth medium in which an organism expressing the protein is cultured. However, for purposes of the present invention, such polypeptides may also be recovered intracellularly. Secretion into growth media is readily determined using a number of detection techniques, including, e.g., polyacrylamide gel electrophoresis and the like, and immunological techniques such as Western blotting and immunoprecipitation assays as described in, e.g., International Publication No. WO 96/04301, published February 15, 1996.

A gp120 or other Env polypeptide is produced "intracellularly" when it is found within the cell, either associated with components of the cell, such as in association with the endoplasmic reticulum (ER) or the Golgi Apparatus, or when it is present in the soluble cellular fraction. The gp120 and other Env polypeptides of the present invention may also be secreted into growth medium so long as sufficient amounts of the polypeptides remain

present within the cell such that they can be purified from cell lysates using techniques described herein.

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An "immunogenic" gp120 or other Env protein is a molecule that includes at least one epitope such that the molecule is capable of either eliciting an immunological reaction in an individual to which the protein is administered or, in the diagnostic context, is capable of reacting with antibodies directed against the HIV in question.

By "epitope" is meant a site on an antigen to which specific B cells and/or T cells respond, rendering the molecule including such an epitope capable of eliciting an immunological reaction or capable of reacting with HIV antibodies present in a biological sample. The term is also used interchangeably with "antigenic determinant" or "antigenic determinant site." An epitope can comprise 3 or more amino acids in a spatial conformation unique to the epitope. Generally, an epitope consists of at least 5 such amino acids and, more usually, consists of at least 8-10 such amino acids. Methods of determining spatial conformation of amino acids are known in the art and include, for example, x-ray crystallography and 2-dimensional nuclear magnetic resonance. Furthermore, the identification of epitopes in a given protein is readily accomplished using techniques well known in the art, such as by the use of hydrophobicity studies and by site-directed serology. See, also, Geysen et al., Proc. Natl. Acad. Sci. USA (1984) 81:3998-4002 (general method of rapidly synthesizing peptides to determine the location of immunogenic epitopes in a given antigen); U.S. Patent No. 4,708,871 (procedures for identifying and chemically synthesizing epitopes of antigens); and Geysen et al., Molecular Immunology (1986) 23:709-715 (technique for identifying peptides with high affinity for a given antibody). Antibodies that recognize the same epitope can be identified in a simple immunoassay showing the ability of one antibody to block the binding of another antibody to a target antigen.

An "immunological response" or "immune response" as used herein is the development in the subject of a humoral and/or a cellular immune response to the Env (e.g., gp120) polypeptide when the polypeptide is present in a vaccine composition. These antibodies may also neutralize infectivity, and/or mediate antibody-complement or antibody dependent cell cytotoxicity to provide protection to an immunized host. Immunological reactivity may be determined in standard immunoassays, such as a competition assays, well known in the art.

Techniques for determining amino acid sequence "similarity" are well known in the art. In general, "similarity" means the exact amino acid to amino acid comparison of two or more polypeptides at the appropriate place, where amino acids are identical or possess similar chemical and/or physical properties such as charge or hydrophobicity. A so-termed "percent similarity" then can be determined between the compared polypeptide sequences.

Techniques for determining nucleic acid and amino acid sequence identity also are well known in the art and include determining the nucleotide sequence of the mRNA for that gene (usually via a cDNA intermediate) and determining the amino acid sequence encoded thereby, and comparing this to a second amino acid sequence. In general, "identity" refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of two polynucleotides or polypeptide sequences, respectively.

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Two or more polynucleotide sequences can be compared by determining their "percent identity." Two or more amino acid sequences likewise can be compared by determining their "percent identity." The percent identity of two sequences, whether nucleic acid or peptide sequences, is generally described as the number of exact matches between two aligned sequences divided by the length of the shorter sequence and multiplied by 100. An approximate alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981). This algorithm can be extended to use with peptide sequences using the scoring matrix developed by Dayhoff, Atlas of Protein Sequences and Structure, M.O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA, and normalized by Gribskov, Nucl. Acids Res. 14(6):6745-6763 (1986). An implementation of this algorithm for nucleic acid and peptide sequences is provided by the Genetics Computer Group (Madison, WI) in their BestFit utility application. The default parameters for this method are described in the Wisconsin Sequence Analysis Package Program Manual, Version 8 (1995) (available from Genetics Computer Group, Madison, WI). Other equally suitable programs for calculating the percent identity or similarity between sequences are generally known in the art.

For example, percent identity of a particular nucleotide sequence to a reference sequence can be determined using the homology algorithm of Smith and Waterman with a default scoring table and a gap penalty of six nucleotide positions. Another method of establishing percent identity in the context of the present invention is to use the MPSRCH

package of programs copyrighted by the University of Edinburgh, developed by John F. Collins and Shane S. Sturrok, and distributed by IntelliGenetics, Inc. (Mountain View, CA). From this suite of packages, the Smith-Waterman algorithm can be employed where default parameters are used for the scoring table (for example, gap open penalty of 12, gap extension penalty of one, and a gap of six). From the data generated, the "Match" value reflects "sequence identity." Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, such as the alignment program BLAST, which can also be used with default parameters. For example, BLASTN and BLASTP can be used with the following default parameters: genetic code = standard; filter = none; strand = both; cutoff = 60; expect = 10; Matrix = BLOSUM62; Descriptions = 50 sequences; sort by = HIGH SCORE; Databases = non-redundant, GenBank + EMBL + DDBJ + PDB + GenBank CDS translations + Swiss protein + Spupdate + PIR. Details of these programs can be found at the following internet address: http://www.ncbi.nlm.gov/cgi-bin/BLAST.

One of skill in the art can readily determine the proper search parameters to use for a given sequence in the above programs. For example, the search parameters may vary based on the size of the sequence in question. Thus, for example, a representative embodiment of the present invention would include an isolated polynucleotide having X contiguous nucleotides, wherein (i) the X contiguous nucleotides have at least about 50% identity to Y contiguous nucleotides derived from any of the sequences described herein, (ii) X equals Y, and (iii) X is greater than or equal to 6 nucleotides and up to 5000 nucleotides, preferably greater than or equal to 8 nucleotides and up to 5000 nucleotides, more preferably 10-12 nucleotides and up to 5000 nucleotides, and even more preferably 15-20 nucleotides, up to the number of nucleotides present in the full-length sequences described herein (e.g., see the Sequence Listing and claims), including all integer values falling within the above-described ranges.

The synthetic expression cassettes (and purified polynucleotides) of the present invention include related polynucleotide sequences having about 80% to 100%, greater than 80-85%, preferably greater than 90-92%, more preferably greater than 95%, and most preferably greater than 98% sequence (including all integer values falling within these described ranges) identity to the synthetic expression cassette sequences disclosed herein (for example, to the claimed sequences or other sequences of the present invention) when the sequences of the present invention are used as the query sequence.

Computer programs are also available to determine the likelihood of certain polypeptides to form structures such as β-sheets. One such program, described herein, is the "ALB" program for protein and polypeptide secondary structure calculation and predication. In addition, secondary protein structure can be predicted from the primary amino acid sequence, for example using protein crystal structure and aligning the protein sequence related to the crystal structure (e.g., using Molecular Operating Environment (MOE) programs available from the Chemical Computing Group Inc., Montreal, P.Q., Canada). Other methods of predicting secondary structures are described, for example, in Garnier et al. (1996) Methods Enzymol. 266:540-553; Geourjon et al. (1995) Comput. Applic. Biosci. 11:681-684; Levin (1997) Protein Eng. 10:771-776; and Rost et al. (1993) J. Molec. Biol. 232:584-599.

Homology can also be determined by hybridization of polynucleotides under conditions which form stable duplexes between homologous regions, followed by digestion with single-stranded-specific nuclease(s), and size determination of the digested fragments. Two DNA, or two polypeptide sequences are "substantially homologous" to each other when the sequences exhibit at least about 80%-85%, preferably at least about 90%, and most preferably at least about 95%-98% sequence identity over a defined length of the molecules, as determined using the methods above. As used herein, substantially homologous also refers to sequences showing complete identity to the specified DNA or polypeptide sequence. DNA sequences that are substantially homologous can be identified in a Southern hybridization experiment under, for example, stringent conditions, as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Sambrook et al., supra; DNA Cloning, supra; Nucleic Acid Hybridization, supra.

A "coding sequence" or a sequence which "encodes" a selected protein, is a nucleic acid sequence which is transcribed (in the case of DNA) and translated (in the case of mRNA) into a polypeptide in vitro or in vivo when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. A coding sequence can include, but is not limited to cDNA from viral nucleotide sequences as well as synthetic and semisynthetic DNA sequences and sequences including base analogs. A transcription termination sequence may be located 3' to the coding sequence.

"Control elements" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the transcription and translation of a coding sequence in a host cell. Not all of these control elements need always be present so long as the desired gene is capable of being transcribed and translated.

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A control element "directs the transcription" of a coding sequence in a cell when RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

"Operably linked" refers to an arrangement of elements wherein the components so described are configured so as to perform their usual function. Thus, control elements operably linked to a coding sequence are capable of effecting the expression of the coding sequence when RNA polymerase is present. The control elements need not be contiguous with the coding sequence, so long as they function to direct the expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between, e.g., a promoter sequence and the coding sequence and the promoter sequence can still be considered "operably linked" to the coding sequence.

"Recombinant" as used herein to describe a nucleic acid molecule means a polynucleotide of genomic, cDNA, semisynthetic, or synthetic origin which, by virtue of its origin or manipulation: (1) is not associated with all or a portion of the polynucleotide with which it is associated in nature; and/or (2) is linked to a polynucleotide other than that to which it is linked in nature. The term "recombinant" as used with respect to a protein or polypeptide means a polypeptide produced by expression of a recombinant polynucleotide. "Recombinant host cells," "host cells," "cells," "cell lines," "cell cultures," and other such terms denoting procaryotic microorganisms or eucaryotic cell lines cultured as unicellular entities, are used interchangeably, and refer to cells which can be, or have been, used as recipients for recombinant vectors or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood that the progeny of a single parental cell may not necessarily be completely identical in morphology or in genomic or total DNA complement to the original parent, due to accidental or deliberate mutation. Progeny of the parental cell which are sufficiently similar to the parent to be characterized by the relevant property, such as the presence of a nucleotide sequence encoding a desired peptide, are included in the progeny intended by this definition, and are covered by the above terms.

By "vertebrate subject" is meant any member of the subphylum chordata, including, without limitation, humans and other primates, including non-human primates such as chimpanzees and other apes and monkey species; farm animals such as cattle, sheep, pigs, goats and horses; domestic mammals such as dogs and cats; laboratory animals including rodents such as mice, rats and guinea pigs; birds, including domestic, wild and game birds such as chickens, turkeys and other gallinaceous birds, ducks, geese, and the like. The term does not denote a particular age. Thus, both adult and newborn individuals are intended to be covered.

As used herein, a "biological sample" refers to a sample of tissue or fluid isolated from an individual, including but not limited to, for example, blood, plasma, serum, fecal matter, urine, bone marrow, bile, spinal fluid, lymph fluid, samples of the skin, external secretions of the skin, respiratory, intestinal, and genitourinary tracts, samples derived from the gastric epithelium and gastric mucosa, tears, saliva, milk, blood cells, organs, biopsies and also samples of *in vitro* cell culture constituents including but not limited to conditioned media resulting from the growth of cells and tissues in culture medium, e.g., recombinant cells, and cell components.

The terms "label" and "detectable label" refer to a molecule capable of detection, including, but not limited to, radioactive isotopes, fluorescers, chemiluminescers, enzymes, enzyme substrates, enzyme cofactors, enzyme inhibitors, chromophores, dyes, metal ions, metal sols, ligands (e.g., biotin or haptens) and the like. The term "fluorescer" refers to a substance or a portion thereof which is capable of exhibiting fluorescence in the detectable range. Particular examples of labels which may be used with the invention include, but are not limited to fluorescein, rhodamine, dansyl, umbelliferone, Texas red, luminol, acradimum esters, NADPH,  $\alpha$ - $\beta$ -galactosidase, horseradish peroxidase, glucose oxidase, alkaline phosphatase and urease.

#### Overview

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The present invention concerns modified Env polypeptide molecules (e.g., glycoprotein ("gp") 120). Without being bound by a particular theory, it appears that it has been difficult to generate immunological responses against Env because the CD4 binding site is buried between the outer domain, the inner domain and the V1/V2 domains. Thus, although deletion of the V1/V2 domain may render the virus more susceptible to

neutralization by monoclonal antibody directed to the CD4 site, the bridging sheet covering most of the CD4 binding domain may prevent an antibody response. Thus, the present invention provides Env polypeptides that maintain their general overall structure yet expose the CD4 binding domain. This allows the generation of an immune response (e.g., an antibody response) to epitopes in or near the CD4 binding site.

Various forms of the different embodiments of the invention, described herein, may be combined.

## **β-Sheet Conformations**

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In the present invention, location of the  $\beta$ -sheet structures were identified relative to 3-D (crystal) structure of an HXB-2 crystallized Env protein (see, Example 1A). Based on this structure, constructs encoding polypeptides having replacements and or excisions which maintain overall geometry while exposing the CD4 binding site were designed. In particular, the crystal structure of HXB-2 was downloaded from the Brookhaven Database. Using the default parameters of the Loop Search feature of the Biopolymer module of the Sybyl molecular modeling package, homology and fit of amino acids which could replace the native loops between  $\beta$ -strands yet maintain overall tertiary structure were determined. Constructs encoding the modified Env polypeptides were then designed (Example 1.B.).

Thus, the modified Env polypeptides typically have enough of the bridging sheet removed to expose the CD4 groove, but have enough of the structure to allow correct folding of the Env glycoprotein. Exemplary constructs are described below.

#### Polypeptide Production

The polypeptides of the present invention can be produced in any number of ways which are well known in the art.

In one embodiment, the polypeptides are generated using recombinant techniques, well known in the art. In this regard, oligonucleotide probes can be devised based on the known sequences of the Env (e.g., gp120) polypeptide genome and used to probe genomic or cDNA libraries for Env genes. The gene can then be further isolated using standard techniques and, e.g., restriction enzymes employed to truncate the gene at desired portions of the full-length sequence. Similarly, the Env gene(s) can be isolated directly from cells and tissues containing the same, using known techniques, such as phenol extraction and the

sequence further manipulated to produce the desired truncations. See, e.g., Sambrook et al., supra, for a description of techniques used to obtain and isolate DNA.

The genes encoding the modified (e.g., truncated and/or substituted) polypeptides can be produced synthetically, based on the known sequences. The nucleotide sequence can be designed with the appropriate codons for the particular amino acid sequence desired. The complete sequence is generally assembled from overlapping oligonucleotides prepared by standard methods and assembled into a complete coding sequence. See, e.g., Edge (1981) Nature 292:756; Nambair et al. (1984) Science 223:1299; Jay et al. (1984) J. Biol. Chem. 259:6311; Stemmer et al. (1995) Gene 164:49-53.

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Recombinant techniques are readily used to clone a gene encoding an Env polypeptide gene which can then be mutagenized *in vitro* by the replacement of the appropriate base pair(s) to result in the codon for the desired amino acid. Such a change can include as little as one base pair, effecting a change in a single amino acid, or can encompass several base pair changes. Alternatively, the mutations can be effected using a mismatched primer which hybridizes to the parent nucleotide sequence (generally cDNA corresponding to the RNA sequence), at a temperature below the melting temperature of the mismatched duplex. The primer can be made specific by keeping primer length and base composition within relatively narrow limits and by keeping the mutant base centrally located. See, *e.g.*, Innis et al, (1990) PCR Applications: Protocols for Functional Genomics; Zoller and Smith, *Methods Enzymol*. (1983) 100:468. Primer extension is effected using DNA polymerase, the product cloned and clones containing the mutated DNA, derived by segregation of the primer extended strand, selected. Selection can be accomplished using the mutant primer as a hybridization probe. The technique is also applicable for generating multiple point mutations. See, e.g., Dalbie-McFarland et al. *Proc. Natl. Acad. Sci USA* (1982) 79:6409.

Once coding sequences for the desired proteins have been isolated or synthesized, they can be cloned into any suitable vector or replicon for expression. As will be apparent from the teachings herein, a wide variety of vectors encoding modified polypeptides can be generated by creating expression constructs which operably link, in various combinations, polynucleotides encoding Env polypeptides having deletions or mutation therein. Thus, polynucleotides encoding a particular deleted V1/V2 region can be operably linked with polynucleotides encoding polypeptides having deletions or replacements in the small loop

region and the construct introduced into a host cell for polypeptide expression. Non-limiting examples of such combinations are discussed in the Examples.

Numerous cloning vectors are known to those of skill in the art, and the selection of an appropriate cloning vector is a matter of choice. Examples of recombinant DNA vectors for cloning and host cells which they can transform include the bacteriophage λ (E. coli), pBR322 (E. coli), pACYC177 (E. coli), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-E. coli gram-negative bacteria), pHV14 (E. coli and Bacillus subtilis), pBD9 (Bacillus), pIJ61 (Streptomyces), pUC6 (Streptomyces), YIp5 (Saccharomyces), YCp19 (Saccharomyces) and bovine papilloma virus (mammalian cells). See, generally, DNA Cloning: Vols. I & II, supra; Sambrook et al., supra; B. Perbal, supra.

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Insect cell expression systems, such as baculovirus systems, can also be used and are known to those of skill in the art and described in, e.g., Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987). Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, inter alia, Invitrogen, San Diego CA ("MaxBac" kit).

Plant expression systems can also be used to produce the modified Env proteins. Generally, such systems use virus-based vectors to transfect plant cells with heterologous genes. For a description of such systems see, e.g., Porta et al., *Mol. Biotech.* (1996) 5:209-221; and Hackland et al., *Arch. Virol.* (1994) 139:1-22.

Viral systems, such as a vaccinia based infection/transfection system, as described in Tomei et al., J. Virol. (1993) 67:4017-4026 and Selby et al., J. Gen. Virol. (1993) 74:1103-1113, will also find use with the present invention. In this system, cells are first transfected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the DNA of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into protein by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation product(s).

The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control" elements), so that the DNA sequence encoding the desired Env polypeptide is transcribed into RNA in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. With the present invention, both the naturally occurring signal peptides or heterologous sequences can be used. Leader sequences can be removed by the host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739; 4,425,437; 4,338,397. Such sequences include, but are not limited to, the TPA leader, as well as the honey bee mellitin signal sequence.

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Other regulatory sequences may also be desirable which allow for regulation of expression of the protein sequences relative to the growth of the host cell. Such regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.

The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.

In some cases it may be necessary to modify the coding sequence so that it may be attached to the control sequences with the appropriate orientation; *i.e.*, to maintain the proper reading frame. Mutants or analogs may be prepared by the deletion of a portion of the sequence encoding the protein, by insertion of a sequence, and/or by substitution of one or more nucleotides within the sequence. Techniques for modifying nucleotide sequences, such as site-directed mutagenesis, are well known to those skilled in the art. See, e.g., Sambrook et al., supra; DNA Cloning, Vols. I and II, supra; Nucleic Acid Hybridization, supra.

The expression vector is then used to transform an appropriate host cell. A number of mammalian cell lines are known in the art and include immortalized cell lines available from the American Type Culture Collection (ATCC), such as, but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), Vero293 cells, as well as others. Similarly, bacterial hosts such as *E. coli*, *Bacillus subtilis*, and *Streptococcus spp.*, will find

use with the present expression constructs. Yeast hosts useful in the present invention include inter alia, Saccharomyces cerevisiae, Candida albicans, Candida maltosa, Hansenula polymorpha, Kluyveromyces fragilis, Kluyveromyces lactis, Pichia guillerimondii, Pichia pastoris, Schizosaccharomyces pombe and Yarrowia lipolytica. Insect cells for use with baculovirus expression vectors include, inter alia, Aedes aegypti, Autographa californica, Bombyx mori, Drosophila melanogaster, Spodoptera frugiperda, and Trichoplusia ni.

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Depending on the expression system and host selected, the proteins of the present invention are produced by growing host cells transformed by an expression vector described above under conditions whereby the protein of interest is expressed. The selection of the appropriate growth conditions is within the skill of the art.

In one embodiment, the transformed cells secrete the polypeptide product into the surrounding media. Certain regulatory sequences can be included in the vector to enhance secretion of the protein product, for example using a tissue plasminogen activator (TPA) leader sequence, a γ-interferon signal sequence or other signal peptide sequences from known secretory proteins. The secreted polypeptide product can then be isolated by various techniques described herein, for example, using standard purification techniques such as but not limited to, hydroxyapatite resins, column chromatography, ion-exchange chromatography, size-exclusion chromatography, electrophoresis, HPLC, immunoadsorbent techniques, affinity chromatography, immunoprecipitation, and the like..

Alternatively, the transformed cells are disrupted, using chemical, physical or mechanical means, which lyse the cells yet keep the Env polypeptides substantially intact. Intracellular proteins can also be obtained by removing components from the cell wall or membrane, e.g., by the use of detergents or organic solvents, such that leakage of the Env polypeptides occurs. Such methods are known to those of skill in the art and are described in, e.g., *Protein Purification Applications: A Practical Approach*, (E.L.V. Harris and S. Angal, Eds., 1990)

For example, methods of disrupting cells for use with the present invention include but are not limited to: sonication or ultrasonication; agitation; liquid or solid extrusion; heat treatment; freeze-thaw; desiccation; explosive decompression; osmotic shock; treatment with lytic enzymes including proteases such as trypsin, neuraminidase and lysozyme; alkali treatment; and the use of detergents and solvents such as bile salts, sodium dodecylsulphate,

Triton, NP40 and CHAPS. The particular technique used to disrupt the cells is largely a matter of choice and will depend on the cell type in which the polypeptide is expressed, culture conditions and any pre-treatment used.

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Following disruption of the cells, cellular debris is removed, generally by centrifugation, and the intracellularly produced Env polypeptides are further purified, using standard purification techniques such as but not limited to, column chromatography, ion-exchange chromatography, size-exclusion chromatography, electrophoresis, HPLC, immunoadsorbent techniques, affinity chromatography, immunoprecipitation, and the like.

For example, one method for obtaining the intracellular Env polypeptides of the present invention involves affinity purification, such as by immunoaffinity chromatography using anti-Env specific antibodies, or by lectin affinity chromatography. Particularly preferred lectin resins are those that recognize mannose moieties such as but not limited to resins derived from *Galanthus nivalis* agglutinin (GNA), *Lens culinaris* agglutinin (LCA or lentil lectin), *Pisum sativum* agglutinin (PSA or pea lectin), *Narcissus pseudonarcissus* agglutinin (NPA) and *Allium ursinum* agglutinin (AUA). The choice of a suitable affinity resin is within the skill in the art. After affinity purification, the Env polypeptides can be further purified using conventional techniques well known in the art, such as by any of the techniques described above.

It may be desirable to produce Env (e.g., gp120) complexes, either with itself or other proteins. Such complexes are readily produced by e.g., co-transfecting host cells with constructs encoding for the Env (e.g., gp120) and/or other polypeptides of the desired complex. Co-transfection can be accomplished either in trans or cis, i.e., by using separate vectors or by using a single vector which bears both of the Env and other gene. If done using a single vector, both genes can be driven by a single set of control elements or, alternatively, the genes can be present on the vector in individual expression cassettes, driven by individual control elements. Following expression, the proteins will spontaneously associate.

Alternatively, the complexes can be formed by mixing the individual proteins together which have been produced separately, either in purified or semi-purified form, or even by mixing culture media in which host cells expressing the proteins, have been cultured. See, International Publication No. WO 96/04301, published February 15, 1996, for a description of such complexes.

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Relatively small polypeptides, i.e., up to about 50 amino acids in length, can be conveniently synthesized chemically, for example by any of several techniques that are known to those skilled in the peptide art. In general, these methods employ the sequential addition of one or more amino acids to a growing peptide chain. Normally, either the amino or carboxyl group of the first amino acid is protected by a suitable protecting group. The protected or derivatized amino acid can then be either attached to an inert solid support or utilized in solution by adding the next amino acid in the sequence having the complementary (amino or carboxyl) group suitably protected, under conditions that allow for the formation of an amide linkage. The protecting group is then removed from the newly added amino acid residue and the next amino acid (suitably protected) is then added, and so forth. After the desired amino acids have been linked in the proper sequence, any remaining protecting groups (and any solid support, if solid phase synthesis techniques are used) are removed sequentially or concurrently, to render the final polypeptide. By simple modification of this general procedure, it is possible to add more than one amino acid at a time to a growing chain, for example, by coupling (under conditions which do not racemize chiral centers) a protected tripeptide with a properly protected dipeptide to form, after deprotection, a pentapeptide. See, e.g., J. M. Stewart and J. D. Young, Solid Phase Peptide Synthesis (Pierce Chemical Co., Rockford, IL 1984) and G. Barany and R. B. Merrifield, The Peptides: Analysis, Synthesis, Biology, editors E. Gross and J. Meienhofer, Vol. 2, (Academic Press, New York, 1980), pp. 3-254, for solid phase peptide synthesis techniques; and M. Bodansky, Principles of Peptide Synthesis, (Springer-Verlag, Berlin 1984) and E. Gross and J. Meienhofer, Eds., The Peptides: Analysis, Synthesis, Biology, Vol. 1, for classical solution synthesis.

Typical protecting groups include t-butyloxycarbonyl (Boc), 925 fluorenylmethoxycarbonyl (Fmoc) benzyloxycarbonyl (Cbz); p-toluenesulfonyl (Tx); 2,4dinitrophenyl; benzyl (Bzl); biphenylisopropyloxycarboxy-carbonyl, tamyloxycarbonyl, isobornyloxycarbonyl, o-bromobenzyloxycarbonyl, cyclohexyl, isopropyl,
acetyl, o-nitrophenylsulfonyl and the like.

Typical solid supports are cross-linked polymeric supports. These can include divinylbenzene cross-linked-styrene-based polymers, for example, divinylbenzene-hydroxymethylstyrene copolymers, divinylbenzene-chloromethylstyrene copolymers and divinylbenzene-benzhydrylaminopolystyrene copolymers.

The polypeptide analogs of the present invention can also be chemically prepared by other methods such as by the method of simultaneous multiple peptide synthesis. See, e.g., Houghten *Proc. Natl. Acad. Sci. USA* (1985) 82:5131-5135; U.S. Patent No. 4,631,211.

#### Diagnostic and Vaccine Applications

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The intracellularly produced Env polypeptides of the present invention, complexes thereof, or the polynucleotides coding therefor, can be used for a number of diagnostic and therapeutic purposes. For example, the proteins and polynucleotides or antibodies generated against the same, can be used in a variety of assays, to determine the presence of reactive antibodies/and or Env proteins in a biological sample to aid in the diagnosis of HIV infection or disease status or as measure of response to immunization.

The presence of antibodies reactive with the Env (e.g., gp120) polypeptides and, conversely, antigens reactive with antibodies generated thereto, can be detected using standard electrophoretic and immunodiagnostic techniques, including immunoassays such as competition, direct reaction, or sandwich type assays. Such assays include, but are not limited to, western blots; agglutination tests; enzyme-labeled and mediated immunoassays, such as ELISAs; biotin/avidin type assays; radioimmunoassays; immunoelectrophoresis; immunoprecipitation, etc. The reactions generally include revealing labels such as fluorescent, chemiluminescent, radioactive, or enzymatic labels or dye molecules, or other methods for detecting the formation of a complex between the antigen and the antibody or antibodies reacted therewith.

Solid supports can be used in the assays such as nitrocellulose, in membrane or microtiter well form; polyvinylchloride, in sheets or microtiter wells; polystyrene latex, in beads or microtiter plates; polyvinylidine fluoride; diazotized paper; nylon membranes; activated beads, and the like.

Typically, the solid support is first reacted with the biological sample (or the gp120 proteins), washed and then the antibodies, (or a sample suspected of containing antibodies), applied. After washing to remove any non-bound ligand, a secondary binder moiety is added under suitable binding conditions, such that the secondary binder is capable of associating selectively with the bound ligand. The presence of the secondary binder can then be detected using techniques well known in the art. Typically, the secondary binder will comprise an antibody directed against the antibody ligands. A number of anti-human immunoglobulin

(Ig) molecules are known in the art (e.g., commercially available goat anti-human Ig or rabbit anti-human Ig). Ig molecules for use herein will preferably be of the IgG or IgA type, however, IgM may also be appropriate in some instances. The Ig molecules can be readily conjugated to a detectable enzyme label, such as horseradish peroxidase, glucose oxidase, Beta-galactosidase, alkaline phosphatase and urease, among others, using methods known to those of skill in the art. An appropriate enzyme substrate is then used to generate a detectable signal.

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Alternatively, a "two antibody sandwich" assay can be used to detect the proteins of the present invention. In this technique, the solid support is reacted first with one or more of the antibodies directed against Env (e.g., gp120), washed and then exposed to the test sample. Antibodies are again added and the reaction visualized using either a direct color reaction or using a labeled second antibody, such as an anti-immunoglobulin labeled with horseradish peroxidase, alkaline phosphatase or urease.

Assays can also be conducted in solution, such that the viral proteins and antibodies thereto form complexes under precipitating conditions. The precipitated complexes can then be separated from the test sample, for example, by centrifugation. The reaction mixture can be analyzed to determine the presence or absence of antibody-antigen complexes using any of a number of standard methods, such as those immunodiagnostic methods described above.

The modified Env proteins, produced as described above, or antibodies to the proteins, can be provided in kits, with suitable instructions and other necessary reagents, in order to conduct immunoassays as described above. The kit can also contain, depending on the particular immunoassay used, suitable labels and other packaged reagents and materials (i.e. wash buffers and the like). Standard immunoassays, such as those described above, can be conducted using these kits.

The Env polypeptides and polynucleotides encoding the polypeptides can also be used in vaccine compositions, individually or in combination, in e.g., prophylactic (i.e., to prevent infection) or therapeutic (to treat HIV following infection) vaccines. The vaccines can comprise mixtures of one or more of the modified Env proteins (or nucleotide sequences encoding the proteins), such as Env (e.g., gp120) proteins derived from more than one viral isolate. The vaccine may also be administered in conjunction with other antigens and immunoregulatory agents, for example, immunoglobulins, cytokines, lymphokines, and chemokines, including but not limited to IL-2, modified IL-2 (cys125-ser125), GM-CSF, IL-

12, γ-interferon, IP-10, MIP1β and RANTES. The vaccines may be administered as polypeptides or, alternatively, as naked nucleic acid vaccines (e.g., DNA), using viral vectors (e.g., retroviral vectors, adenoviral vectors, adeno-associated viral vectors) or non-viral vectors (e.g., liposomes, particles coated with nucleic acid or protein). The vaccines may also comprise a mixture of protein and nucleic acid, which in turn may be delivered using the same or different vehicles. The vaccine may be given more than once (e.g., a "prime" administration followed by one or more "boosts") to achieve the desired effects. The same composition can be administered as the prime and as the one or more boosts. Alternatively, different compositions can be used for priming and boosting.

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The vaccines will generally include one or more "pharmaceutically acceptable excipients or vehicles" such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

A carrier is optionally present which is a molecule that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycollic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Furthermore, the Env polypeptide may be conjugated to a bacterial toxoid, such as toxoid from diphtheria, tetanus, cholera, etc.

Adjuvants may also be used to enhance the effectiveness of the vaccines. Such adjuvants include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc.; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (International Publication No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size

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emulsion, and (c) Ribi<sup>TM</sup> adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox<sup>TM</sup>); (3) saponin adjuvants, such as Stimulon<sup>TM</sup> (Cambridge Bioscience, Worcester, MA) may be used or particle generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freunds Adjuvant (CFA) and Incomplete Freunds Adjuvant (IFA); (5) cytokines, such as interleukins (IL-1, IL-2, etc.), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc.; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an E. coli heat-labile toxin (LT), particularly LT-K63 (where lysine is substituted for the wild-type amino acid at position 63) LT-R72 (where arginine is substituted for the wild-type amino acid at position 72), CT-S109 (where serine is substituted for the wild-type amino acid at position 109), and PT-K9/G129 (where lysine is substituted for the wild-type amino acid at position 9 and glycine substituted at position 129) (see, e.g., International Publication Nos. W093/13202 and W092/19265); and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition.

Muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acteyl-normuramyl-L-alanyl-D-isogluatme (nor-MDP), N-acetylmuramyl-L-alanyl-D-isogluatminyl-L-alanine-2-(l'-2'-dipalmitoyl-sn-glycero-3-huydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

Typically, the vaccine compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above.

The vaccines will comprise a therapeutically effective amount of the modified Env proteins, or complexes of the proteins, or nucleotide sequences encoding the same, and any other of the above-mentioned components, as needed. By "therapeutically effective amount" is meant an amount of a modified Env (e.g., gp120) protein which will induce a protective immunological response in the uninfected, infected or unexposed individual to which it is administered. Such a response will generally result in the development in the subject of a secretory, cellular and/or antibody-mediated immune response to the vaccine. Usually, such

a response includes but is not limited to one or more of the following effects; the production of antibodies from any of the immunological classes, such as immunoglobulins A, D, E, G or M; the proliferation of B and T lymphocytes; the provision of activation, growth and differentiation signals to immunological cells; expansion of helper T cell, suppressor T cell, and/or cytotoxic T cell.

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Preferably, the effective amount is sufficient to bring about treatment or prevention of disease symptoms. The exact amount necessary will vary depending on the subject being treated; the age and general condition of the individual to be treated; the capacity of the individual's immune system to synthesize antibodies; the degree of protection desired; the severity of the condition being treated; the particular Env polypeptide selected and its mode of administration, among other factors. An appropriate effective amount can be readily determined by one of skill in the art. A "therapeutically effective amount" will fall in a relatively broad range that can be determined through routine trials.

Once formulated, the nucleic acid vaccines may be accomplished with or without viral vectors, as described above, by injection using either a conventional syringe or a gene gun, such as the Accell® gene delivery system (PowderJect Technologies, Inc., Oxford, England). Delivery of DNA into cells of the epidermis is particularly preferred as this mode of administration provides access to skin-associated lymphoid cells and provides for a transient presence of DNA in the recipient. Both nucleic acids and/or peptides can be injected either subcutaneously, epidermally, intradermally, intramucosally such as nasally, rectally and vaginally, intraperitoneally, intravenously, orally or intramuscularly. Other modes of administration include oral and pulmonary administration, suppositories, needle-less injection, transcutaneous and transdermal applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. Administration of nucleic acids may also be combined with administration of peptides or other substances.

While the invention has been described in conjunction with the preferred specific embodiments thereof, it is to be understood that the foregoing description as well as the examples which follow are intended to illustrate and not limit the scope of the invention. Other aspects, advantages and modifications within the scope of the invention will be apparent to those skilled in the art to which the invention pertains.

#### Experimental

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Below are examples of specific embodiments for carrying out the present invention. The examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperatures, etc.), but some experimental error and deviation should, of course, be allowed for.

#### EXAMPLE 1

10 A.1. Best-Fit and Homology Searches

The crystal structure of HXB-2 gp 120 was downloaded from the Brookhaven database (COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) 15-JUN-98 1GC1 TITLE: HIV-1 GP120 CORE COMPLEXED WITH CD4 AND A NEUTRALIZING HUMAN ANTIBODY). Beta strands 3, 2, 21, and 20 of gp 120 form a sheet near the CD4 binding site. Strands β-3 and β-2 are connected by the V1/V2 loop. Strands β-21 and β-20 are connected by another small loop. The H-bonds at the interface between strands β-2 and β-21 are the only connection between domains of the "lower" half of the protein (joining helix alpha 1 to the CD4 binding site). This beta sheet and these loops mask some antigens (e.g., antigens which may generate neutralizing antibodies) that are only exposed during the CD4 binding.

Constructs that remove enough of the beta sheet to expose the antigens in the CD4 binding site, but leave enough of the protein to allow correct folding were designed.

Specifically targeted were modifications to the small loop and, optional deletion of the V1/V2 loops. Three different types of constructs were designed: (1) constructs encoding polypeptides that leave the number of residues making up the entire 4-strand beta sheet intact, but replace one or more residues; (2) constructs that encode polypeptide having at least one residue of at least one beta strand excised or (3) constructs encoding polypeptides having at least two residues of at least one beta strand excised. Thus, a total of 6 different turns were needed to rejoin the ends of the strands.

Initially, residues in the small loop (residues 427-430, relative to HXB-2) and connected beta strands ( $\beta$ -20 and  $\beta$ -21) were modified to contain Gly and Pro (common in beta turns). These sequences were then used as the target to match in each search. The

geometry of the target was matched to known proteins in the Brookhaven Protein Data Bank. In particular, 5-residue turns (including an overlapping single residue at the N-terminal, the 2 residue target turn and 2 overlapping residues at the C-terminal) were searched in the databases. In other words, these modified loops add a 2 residue turn that should be able to support a geometry that will maintain the beta-sheet structure of the wild type protein. The calculations were performed using the default parameters in the Loop Search feature of the Biopolymer module of the Sybyl molecular modeling package. In each case, the 25 best fits based on geometry alone were reviewed and, of those, several selected for homology and fit.

In addition, it was also determined what modifications could be made to remove most of the V1/V2 loop (residues 124-198, relative to HXB-2) yet leave the geometry of the protein intact. As with the small loop, constructs were also designed which excised one or more residues from the  $\beta$ -2 strand (residues 119-123 of HXB-2), the  $\beta$ -3 strand (residues 199-201 of HXB-2) or both  $\beta$ -2 and  $\beta$ -3. For these constructs, known loops were searched to match the geometry of a pentamer (including two remaining residues from the N-terminal side, a 2 residue turn and 1 C-terminal residue). For these searches, Gly-Gly was preferred as the insert along with at least one C-terminal substitution.

## A.2. Small Loop Replacements

In one aspect, the native sequence was replaced with residues that expose the CD4 binding site, but leave the overall geometry of the protein relatively unchanged. For the small loop replacements, the target to match was: ASN425-MET426-GLY427-GLY428-GLY431. Results of the search are summarized in Table 1.

Table 1: Search of Small Loop (Asn425 through Gly431)

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Rank	Sequence	RMSD	% Homology	Seq Id No.
Best fit	LYS-ASP-SER-ASN-ASN	0.16689	62.5	27
3	TYR-GLY-LEU-GLY-LEU	0.220308	62.5	28
4	GLU-ARG-GLU-ASP-GLY	0.241754	62.5	29
7	ARG-LYS-GLY-GLY-ASN	0.24881	100	30
12	TRP-THR-GLY-SER-TYR	0.26417	83.33	31

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Based on these results, constructs encoding Gly-Gly (#7), Gly-Ser (#12) or Gly-Gly-Asn (#7) were recommended.

As V1/V2 and one or more residues of  $\beta$ -2 and  $\beta$ -3 are also optionally deleted in the modified polypeptides of the invention, known loops to match the geometry of the V1/V2 loop were also searched. The V1/V2 loop the target to match was: Lys121-Leu-122-Gly123-Gly124-Ser199. Some notable matches are shown in Table 2:

Table 2: Search of V1/V2 loop (Lys121 through Ser199)

Rank	Sequence	RMSD	% Homology	Seq Id. No.
Best fit	GLN-VAL-HIS-ASP-GLU	0.154764	68.75	32
2	LYS-GLU-GLY-ASP-LYS	0.15718	81.25	33
9	ARG-SER-GLY-ARG-SER	0.173731	68.75	34
11	THR-LEU-GLY-ASN-SER	0.175554	81.25	35
16	HIS-PHE-GLY-ALA-GLY	0.178772	93.75	36

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Based on these searches, constructs encoding Gly-Asn in place of V1/V2 were recommended.

# A.3. One Additional Residue Excisions

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For a slightly truncated small loop, one more residue was trimmed from each beta strand to slightly shorten the beta sheet. The target to match was: ILE424-ASN425-GLY426-GLY427-LYS432. Results are shown in Table 3:

Table 3: Search of Beta sheet shortened by One residue (Ile424 through Lys432)

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Rank	Sequence	RMSD	% Homology	Seq Id No.
Best fit:	ARG-MET-ALA-PRO-VAL	0.316805	58.33	37
Best	ASP-SER-ASP-GLY-PRO	0.440896	83.33	38
hom:				

Although these searches showed more variation and worse fits than the previous truncation, the Pro-Val or Pro-Leu encoding constructs were very similar. Accordingly, Ala-Pro encoding constructs were recommended.

Sequences encoding gp120 polypeptides having V1/V2 deleted and an additional residue from  $\beta$ -2 or  $\beta$ -3 excised were also searched. The V1/V2 loop the target to match was: VAL120-LYS121-GLY122-GLY123-VAL200. Some notable matches are shown in Table 4.

Table 4: Search of V1/V2 loop (Val120 through Val200)

10	Rank	Sequence	RMSD	% Homology	Seq Id No
	Best fit:	THR-VAL-ASP-PRO-TYR	0.400892	58.33333	39
	2	SER-THR-ASN-PRO-LEU	0.402575	54.16667	40
	3	THR-ARG-SER-PRO-LEU	0.403965	58.33333	41
	7	ARG-MET-ALA-PRO-VAL	0.440118	58.33333	42

The construct encoding Ala-Pro (e.g., #7) was recommended.

### A.4. Further Excisions

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In yet another truncation, an additional residue was trimmed from the  $\beta$ -20 and  $\beta$ -21 strands to further shorten the beta sheet. The target to match was ILE423-ILE424-GLY425-GLY426-ALA433. Notable matches are shown in Table 5.

Table 5: Search of Beta sheet shortened by Two Residues (Ile423 through Ala433)

Rank .	Sequence	RMSD	% Homology	Seq Id No
Best fit:	THR-TYR-GLU-GLY-VAL	0.130107	79.16666	43
2	GLN-VAL-GLY-ASN-THR	0.138245	79.16666	44
3:	THR-VAL-GLY-GLY-ILE	0.153362	100	45

A construct encoding Gly-Gly (e.g., #3), which has 100% homology, was recommended.

Also searched were sequences encoding a deleted V1/V2 region and at least two residues excised from  $\beta$ -2,  $\beta$ -3 or at least one residue excised from  $\beta$ -2 and  $\beta$ -3. The target to match was: CYS119-VAL120-GLY121-GLY122-ILE201. Notable matches are shown in Table 6.

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Table 6: Search of V1/V2 loop (Cys119 through Ile201)

Rank	Sequence	RMSD	% Homology	Seq Id No
Best fit:	ASP-LEU-PRO-GLY-CYS	0.250501	75	46
4	ASP-VAL-GLY-GLY-LEU	0.290383	100	47

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It was determined that both constructs would be used.

## B.1. Constructs encoding modified Env polypeptides

As described above, the native loops extruding from the 4-β antiparallel-stands were excised and replaced with 1 to 3 residue turns. The loops were replaced so as to leave the entire β-strands or excised by trimming one or more amino acid from each side of the connected strands. The ends of the strands were rejoined with turns that preserve the same backbone geometry (e.g., tertiary structure of β-20 and β-21), as determined by searching the Brookhaven Protein Data Bank.

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Table 7A is a summary of the truncations of the variable regions 1 and 2 recommended for this study, as determined in Example 1.A. above.

Table 7A

V1/V2 Modifications	SEQ ID NO	Figure
-LEU122-GLY-ASN-SER199	7	10
-LYS121-ALA-PRO-VAL200-	6	9
-VAL120-GLY-GLY-ILE201-	4	7
-VAL120-PRO-GLY-ILE201B-	5	8
-VAL120-GLY-ALA-GLY-ALA204-	3	6
-VAL120-GLY-GLY-ALA-THR202-	8	11
-VAL127-GLY-ALA-GLY-ASN195-	25	28

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As previously noted, the polypeptides encoded by the constructs of the present invention are numbered relative to HXB-2, but the particular amino acid residue of the polypeptides encoded by these exemplary constructs is based on SF-162. Thus, for example, although amino acid residue 195 in HXB-2 is a serine (S), constructs encoding polypeptides having then wild type SF162 sequence will have an asparagine (N) at this position. Table 7B shows just three of the variations in amino acid sequence between strains HXB-2 and SF162. The entire sequences, including differences in residue and amino acid number, of HXB-2 and SF162 are shown in the alignment of Figure 2 (SEQ ID NOs:1 and 2).

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Table 7B

HXB-2 amino acid number	HXB-2 Residue	SF162 Residue/amino acid number	
128	Serine (S)	Thr (T)/114	
195	Serine (S)	Asn (N)/188	
426	Met (M)	Arg (R)/411	

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Constructs containing deletions in the  $\beta$ -20 strand,  $\beta$ -21 stand and small loop were also constructed. Shown in Table 8 are constructs encoding truncations in these regions. The constructs in Table 8 are numbered relative to HXB-2 but the unmodified amino acid sequence is based on SF162. Thus, the construct encodes an arginine (Arg) as is found in

SF162 in the amino acid position numbered 426 relative to HXB-2 (See, also, Table 7B). Changes from wildtype (SF162) are shown in bold in Table 8B.

Table 8

Figure SEQ ID NO Small Loop/ $\beta$ -20 and  $\beta$ -21 (Modified) 12 9 -TRP427-GLY-GLY431-13 10 -ARG426-GLY-GLY-GLY431-14 11 -ARG426-GLY-SER-GLY431B-12 15 -ARG426-GLY-GLY-ASN-LYS432-16 13 -ASN425-ALA-PRO-LYS432-17 14 -ILE424-GLY-GLY-ALA433-18 15 -ILE423-GLY-GLY-MET434-GLN422-GLY-GLY-TYR435-16 19 20 17 -GLN422-ALA-PRO-TYR435B-

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The deletion constructs shown in Tables 7 and 8 for each one of the β-strands and combinations of them are constructed. These deletions will be tested in the Env forms gp120, gp140 and gp160 from different HIV strains like subtype B strains (e.g., SF162, US4, SF2), subtype E strains (e.g., CM235) and subtype C strains (e.g., AF110968 or AF110975).

20 Exemplary constructs for SF162 are shown in the

Figures and are summarized in Table 9. As noted above in Figure 2 and Table 7B, in the bridging sheet region, the amino acid sequence of SF162 differs from HXB-2 in that the Met426 of HXB-2 is an Arg in SF162. In Table 9, V1/V2 refers to deletions in the V1/V2 region; # bsm refers to a modification in the bridging sheet small loop.

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Table 9				
Construct	Seq. Id.	Fig.	Modification/Amino acid sequence	
Val120-Ala204	3	6	V1/V2: Val120-Gly-Ala-Gly-Ala204	
Val120-Ile201	4	7 .	V1/V2: Val120-Gly-Gly-Ile201	
Val120-Ile201B	5	8	V1/V2: Val120-Pro-Gly-Ile201	
Lys121-Val200	6	9	V1/V2: Lys121-Ala-Pro-Val200	

		T	able 9
Construct	Seq. Id.	Fig.	Modification/Amino acid sequence
Leu122-Ser199	7	10	V1/V2: Leul 22-Gly-Asn-Ser199
Val120-Thr202	8	11	V1/V2: Val120-Gly-Gly-Ala-Thr202
Trp427-Gly431	9	12	bsm: Trp427-Gly-Gly431
Arg426-Gly431	10	13	bsm: Arg426-Gly-Gly-Gly431
Arg426-Gly431B	11	14	bsm: Arg426-Gly-Ser-Gly431
Arg426-Lys432	12	15	bsm: Arg426-Gly-Gly-Asn-Lys432
Asn425-Lys432	13	16	bsm: Asn425-Ala-Pro-Lys432
Ile424-Ala433	14	17	bsm: Ile424-Gly-Gly-Ala433
Ile423-Met434	15	18	bsm: Ile423-Gly-Gly-Met434
Gln422-Tyr435	16	19	bsm: Gln422-Gly-Gly-Tyr435
Val127-Asn195	25	28	bsm: Val127-Gly-Ala-Gly-Asn195
Gln422-Tyr435B	17	20	bsm: Gln422-Ala-Pro-Tyr435
Leu122-Ser199; Arg426-Gly431	18	21	V1/V2/bsm: Leu122-Gly-Asn-Ser199 Arg4 Gly-Gly-Gly431
Leu122-Ser199; Arg426-Lys432	19	22	V1/V2/bsm: Leu122-Gly-Asn-Ser199 Arg4 Gly-Gly-Asn-Lys432
Leu122-Ser199-Trp427- Gly431	20	23	V1/V2/bsm: Leu122-Gly-Asn-Ser199 Trp4 Gly-Gly431
Lys121-Val200- Asn425-Lys432	21	24	V1/V2/bsm: Lys121-Ala-Pro-Val200 Asn4 Ala-Pro-Lys432
Val120-Ile201-Ile424- Ala433	22	25	V1/V2/bsm: Val120-Gly-Gly-Ile201 Ile424 Gly-Gly-Ala433
Val120-Ile201B-Ile424- Ala433	23	26	V1/V2/bsm: Val120-Pro-Gly-Ile201 Ile424 Gly-Gly-Ala43
Val120-Thr202; Ile424- Ala433	24	27	V1/V2/bsm: Val120-Gly-Gly-Ala-Thr202 lle424-Gly-Gly-Ala433
Val127-Asn195; Arg426-Gly431	25	29	V1/V2/bsm: Val127-Gly-Ala-Gly-Asn195 Arg426-Gly-Gly-Gly431

Combinations of V1/V2 deletions and bridging sheet small loop modifications in addition to those specifically shown in Table 9 are also within the scope of the present invention. Various forms of the different embodiments of the invention, described herein, may be combined.

The first screening will be done after transient expression in COS-7, RD and/or 293 cells. The proteins that are expressed will be analyzed by immunoblot, ELISA, and for binding to mAbs directed to the CD4 binding site and other important epitopes on gp120 to determine integrity of structure. They will also be tested in a CD4 binding assay and, in addition, the binding of neutralizing antibodies, for example using patient sera or mAb 448D (directed to Glu370 and Tyr384, a region of the CD4 binding groove that is not altered by the deletions).

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The immunogenicity of these novel Env glycoproteins will be tested in rodents and primates. The structures will be administered as DNA vaccines or adjuvanted protein vaccines or in combined modalities. The goal of these vaccinations will be to archive broadly reactive neutralizing antibody responses.

## Claims:

## What is claimed is:

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- 1. A polynucleotide encoding a modified HIV Env polypeptide wherein the polypeptide has at least one amino acid deleted or replaced in the region corresponding to residues 420 to 436 relative to HXB-2 (SEQ ID NO:1).
- 2. The polynucleotide of claim 1, wherein the region corresponding to residues 12410 198 relative to HXB-2 is deleted and at least one amino acid is deleted or replaced in the regions corresponding to the residues 119 to 123 and 199 to 210 relative to HXB-2 (SEQ ID NO:1).
- 3. The polynucleotide of claim 1, wherein at least one amino acid in the region corresponding to residues 427 through 429 relative to HXB-2 (SEQ ID NO:1) is deleted or replaced.
  - 4. The polynucleotide of claim 2, wherein at least one amino acid of the in the region corresponding to residues 427 through 429 relative to HXB-2 (SEQ ID NO:1) is deleted or replaced.
    - 5. The polynucleotide of claim 1, wherein the amino acid sequence of the modified HIV Env polypeptide is based on strain SF162.
- 6. An immunogenic modified HIV Env polypeptide having at least one amino acid deleted or replaced in the region corresponding to residues 420 through 436, relative to HXB-2 (SEQ ID NO:1).
- 7. The polypeptide of claim 6, wherein one amino acid is deleted in the region corresponding to residues 420 through 436, relative to HXB-2 (SEQ ID NO:1).

8. The polypeptide of claim 6, wherein more than one amino acid is deleted in the region corresponding to residues 420 through 436, relative to HXB-2 (SEQ ID NO:1).

- 9. The polypeptide of claim 6, wherein at least one amino acid is replaced in the region corresponding to residues 420 through 436, relative to HXB-2 (SEQ ID NO:1).
  - 10. The polypeptide of claim 6, wherein at least one amino acid residue between about amino acid residue 427 and amino acid residue 429 relative to HXB-2 (SEQ ID NO:1) is deleted or replaced.

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- 11. The polypeptide of claim 6, wherein the V1 and V2 regions of the polypeptide are truncated.
- 12. The polypeptide of claim 10, wherein the V1 and V2 regions of the polypeptideare truncated.
  - 13. The polypeptide of claim 6, wherein the amino acid sequence of the modified HIV Env polypeptide is based on strain SF162.
- 14. A construct comprising the nucleotide sequence depicted in Figure 6 (SEQ ID NO:3).
  - 15. A construct comprising the nucleotide sequence depicted in Figure 7 (SEQ ID NO:4).

- 16. A construct comprising the nucleotide sequence depicted in Figure 8 (SEQ ID NO:5).
- 17. A construct comprising the nucleotide sequence depicted in Figure 9 (SEQ ID30 NO:6).

18. A construct comprising the nucleotide sequence depicted in Figure 10 (SEQ ID NO:7).

- 19. A construct comprising the nucleotide sequence depicted in Figure 11 (SEQ ID5 NO:8).
  - 20. A construct comprising the nucleotide sequence depicted in Figure 12 (SEQ ID NO:9).
- 21. A construct comprising the nucleotide sequence depicted in Figure 13 (SEQ ID NO:10).

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- 22. A construct comprising the nucleotide sequence depicted in Figure 14 (SEQ ID NO:11).
- 23. A construct comprising the nucleotide sequence depicted in Figure 15 (SEQ ID NO:12).
- 24. A construct comprising the nucleotide sequence depicted in Figure 16 (SEQ IDNO:13).
  - 25. A construct comprising the nucleotide sequence depicted in Figure 17 (SEQ ID NO:14).
- 25 26. A construct comprising the nucleotide sequence depicted in Figure 18 (SEQ ID NO:15).
  - 27. A construct comprising the nucleotide sequence depicted in Figure 19 (SEQ ID NO:16).
  - 28. A construct comprising the nucleotide sequence depicted in Figure 20 (SEQ ID NO:17).

29. A construct comprising the nucleotide sequence depicted in Figure 21 (SEQ ID NO:18).

- 30. A construct comprising the nucleotide sequence depicted in Figure 22 (SEQ IDNO:19).
  - 31. A construct comprising the nucleotide sequence depicted in Figure 23 (SEQ ID NO:20).
- 32. A construct comprising the nucleotide sequence depicted in Figure 24 (SEQ ID NO:21).
  - 33. A construct comprising the nucleotide sequence depicted in Figure 25 (SEQ ID NO:22).
  - 34. A construct comprising the nucleotide sequence depicted in Figure 26 (SEQ ID NO:23).
- 35. A construct comprising the nucleotide sequence depicted in Figure 27 (SEQ ID NO:24).

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- 36. A construct comprising the nucleotide sequence depicted in Figure 28 (SEQ ID NO:25).
- 25 37. A construct comprising the nucleotide sequence depicted in Figure 29 (SEQ ID NO:26).
  - 38. A vaccine composition comprising a polynucleotide encoding a modified Env polypeptide according to any one of claims 1-5.
  - 39. A vaccine composition comprising a polynucleotide construct encoding a modified Env polypeptide according to any of claims 14-37.

40. A vaccine composition comprising a modified Env polypeptide according to any of claims 6-13.

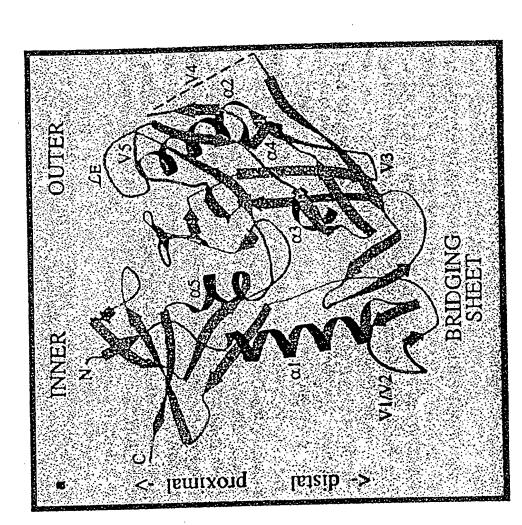
- 41. The vaccine composition of any of claims 38-40, further comprising an adjuvant.
- 42. A method of inducing an immune response in subject comprising, administering a polynucleotide according to any one of claims 1-5 in an amount sufficient to induce an immune response in the subject.

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- 43. A method of inducing an immune response in subject comprising, administering a polynucleotide construct according to any one of claims 14-37 in an amount sufficient to induce an immune response in the subject.
- 44. A method of inducing an immune response in a subject comprising administering a composition comprising a modified Env polypeptide according to any one of claims 6-13, wherein the composition is administered in an amount sufficient to induce an immune response in the subject
- 45. The method of any of claims 42-44 further comprising administering an adjuvant to the subject.
  - 46. A method of inducing an immune response in a subject comprising
  - (a) administering a first composition comprising a polynucleotide according to any of claims 1-5 in a priming step and
  - (b) administering a second composition comprising a modified Env polypeptide according to any of claims 6-13, as a booster, in an amount sufficient to induce an immune response in the subject.
- 47. The method of claim 46 wherein the first composition or second composition further comprise an adjuvant.

48. The method of claim 46 wherein the first and second compositions further comprise an adjuvant.

## ap120 core structure



```
400
                                                                                                                  (323) E-GNMROAHENMSRAKWNNTEKOIASKEREQEGNAKUMIEKOSKERIPSI
                                                  HXB2
                                                                                                                   (314) TIGDIROGHENESGEKANNTIKOIVT GOAQEG-NATERIEKQS SEGIP 3
                                                            162
                                                                                                                  (324) IIGDIRKEHENESRAQUNNTEEDIVKEIREQEGNIKUVAANQSEGUPEN
                                                            SF2
                                                                                                               (324) TIGDIRKENGERNGTKUNEVIT WIE KEKEHEN-NKWII TOPP SEGULET
                                        CM236
                                                                                                                  (334) EIEDIROCHUNESKANNTNTHEDIVEKERECEGNIKTTIENSSSEGUPET
                                                            US4
                                                                                                                (351) IIGDIRQAHCNISRAKWNNTL QIV KLREQFGNNKTIIFNQSSGGDPEI
Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              •450
                                                                                                                                                                                401
                                                                                                                   (372) VTHS ENGGEREZ COSTO TO SEWFNSTWS FEGSINTEGSD TO THE REK
                                                  HXB2
                                                                                                                  (363) VMHS TOGENEROWS TO SENS W-NN--- TIGPNNTNG-- TITE TO RUK
                                                            162
                                                                                                                (374) VMESTNER CETTY ON THE WRLN--HEEG---TKGND I REGERMAN
                                                            SF2
                                                                                                                (373) TMHHENORGE XONTTRONNICIEN--GIMG--GCNG--TEI PLEKOK
                                        CM236
                                                                                                                  (384) VFESTNEGGEREXENT OF STATE OF STAT
                                                            US4
                                                                                                                  (401) VMHSFNCGGEFFYCNTTQLFNSTW N TEG N T G DTIILPCRIK
 Consensus
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                                                                                                                                                                             451
                                                                                                                  (422) YOR MYOKYCKAN APPASSO ARES STANIEL STRIKEG---NSNN HOE
                                                  HXB2
                                                                                                                  (407) OTON RWOEVEK MYADERIRGO ROS HARGL MARKEK-ERSNIT
                                                            162
                                                                                                                  (419) MENMOCEVER MANAGER GEORGE SENERGL GRADING T-NAMEND T-NAMEN DET
                                                            SF2
                                                                                                                CM236
                                                                                                                  (430) DIGENMONEVEKANDENSEN REGUERES SKREWELLEDE STEEN THE TEXT
                                                            US4
                                                                                                                (451) QIINMWQEVGKAMYAPPI GQIRCSSNITGLLLTRDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NITNDTEIF
 Consensus
                                                                                                                (469) RECCEDMR INDUSES FOR SAVE VICTOR KAKARAMO ASKRAUGI-ST
                                                  HXB2
                                                                                                                  (455) RECEIOMRENWESS TO CANVILLA STORY SELLAND RECEIVED THE SE
                                                            162
                                                                                                                  (467) SRENGDMR DARREST TO RECOVER BY THE STREET OF THE STR
                                                            SF2
                                                                                                                  (464) REGENERONGESE CONTROL OF THE C
                                         CM236
                                                                                                                  (480) REGRENM CONTROL VILLE VILLE OF THE CONTROL OF
                                                            US4
                                                                                                                  (501) RPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGI GA
 Consensus
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                                                                                                                                                                           551
                                                                                                                (518) (FL etalerty/telsus/(c/A) stours respector: Sepulsion basis stable of the contract of th
                                                  HXB2
                                                                                                                (504) MFL 32-32-ANSINCIGHTR DEBROOKS TO THE PROPERTY OF THE PR
                                                            162
                                                                                                                (517) MFL CONTRACTOR MONEY STORE (CONTRACTOR OF CONTRACTOR OF CONTRACTOR
                                                            SF2
                                                                                                                (513) MIF STREET ASSISTMENT ASSISTMENT OF THE COURSE STREET ASSISTMENT ASSIST
                                        CM236
                                                                                                                (529) IF CORRECTIVE TO A STREET TO A STREE
                                                           US4
                                                                                                                (551) MFLGFLGAAGSTMGAASLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQ
Consensus
                                                                                                                                                                            601
                                                                                                                (568) MANYIERAGEROLIGITATE SEE KEEQL IGI NCCESSER LEGINALISMAS ISNK
                                                  HXB2
                                                                                                                (554) GROWE KOROSRV WARRANDOOL SEI REGISKL SOM AVENNAS WENK
                                                            162
                                                                                                               (567) HEVITES KIGIFOAR V HAS HELD OLUC I NEGOCIAL KENTAVEWNAS WENK
                                                           SF2
                                                                                                               (563) BIVANCTICKOLOATIV CEVIATRANKOOKE ACHTACHECHECHECHECHENAVRANKSWATEN
                                        CM236
                                                                                                               (579) MANAGER CONFORMATION AND AND COLUMN THE THEORY OF THE PROPERTY OF THE PR
                                                            US4
                                                                                                               (601) LTVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNK
 Consensus
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FIG. 2B

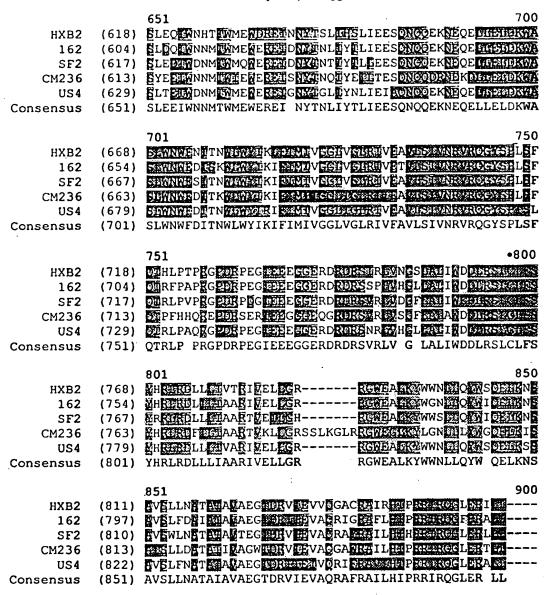


FIG. 2C

Val120-Ile201B	(241)	GAGATCGTGCTGAGAACGTGACCGAGAACTTCAACATGT
Val120-Ala204	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGT
Val120-Ile201	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGT
Val120-Thr202	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGT
Lys121-Val200	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGT
Consensus	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGT
		281 320
Leu122-Ser199	(281)	GGAAGAACAACATGGTGGAGCAGATGCACGAGGACATCAT
Val127-Asn195	(281)	GGAAGAACAACATGGTGGAGCAGATGCACGAGGACATCAT
Val120-Ile201B	(281)	GGAAGAACAACATGGTGGAGCAGATGCACGAGGACATCAT
Val120-Ala204	(281)	GGAAGAACAACATGGTGGAGCAGATGCACGAGGACATCAT
Val120-Ile201	(281)	GGAAGAACATGGTGGAGCAGATGCACGAGGACATCAT
Val120-Thr202	(281)	GGAAGAACAACATGGTGGAGCAGATGCACGAGGACATCAT
Lys121-Val200	(281)	GGAAGAACAACATGGTGGAGCAGATGCACGAGGACATCAT
Consensus	(281)	GGAAGAACAACATGGTGGAGCAGATGCACGAGGACATCAT
0000	,	321
Leu122-Ser199	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG
Val127-Asn195	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTG
Val120-Ile201B	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGCC
Val120 -Ala204	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGG
Val120-11e201	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGG
Val120-Thr202	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGG
Lys121-Val200	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGG
Consensus	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTG
20113211343	(,	361 400
Leu122-Ser199	(361)	CAGCG
Val127-Asn195	(361)	ACCCCCTGTGCGTGGGGGGGGGGAACTGCAACACCAGCG
Val120-Ile201B	(357)	CG
ANTITOTITECATE		
	(357)	
Val120-Ala204		CG
Val120-Ala204 Val120-Ile201	(357)	CG
Val120-Ala204 Val120-Ile201 Val120-Thr202	(357) (357)	cG
Val120-Ala204 Val120-Ile201	(357) (357) (357)	CG CCCCG CCCCCG
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus	(357) (357) (357) (359) (361)	CGCGCCCCG CG 401 440
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus Leu122-Ser199	(357) (357) (357) (359) (361)	
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus Leu122-Ser199 Val127-Asn195	(357) (357) (357) (359) (361) (371) (401)	CGCG
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus Leu122-Ser199 Val127-Asn195 Val120-Ile201B	(357) (357) (357) (359) (361) (371) (401) (359)	
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus Leu122-Ser199 Val127-Asn195	(357) (357) (357) (359) (361) (371) (401) (359) (357)	
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus Leu122-Ser199 Val127-Asn195 Val120-Ile201B	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359)	
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204 Val120-Ile201 Val120-Thr202	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (359)	
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204 Val120-Ile201	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (359) (365)	
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204 Val120-Ile201 Val120-Thr202	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (359)	CG  CG  CG  401  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT CGCCGCCGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCGCCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (359) (365) (401)	
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (359) (365) (401)	CGCATCACCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT CGCCGGCGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  441  480  CCCCATCACTACTGCGCCCCCGCGCCTTCGCCATCCTG
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (365) (401) (411) (441)	CGCATCACTACTGCGCCCGAGGTTCGCCATCGG  CCGCCCATCACTCCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  CATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  CCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  CCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  CCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  CCCCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  CCCCATCCACTAGTGCGCCCCCAGGTGAGCTTCGCCATCCTG
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (365) (401) (411) (441) (399)	CG  CG  CG  CG  401  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT CGCCGGCGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCGCCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  441  480  CCCCATCCACTAGTGCGCCCCGCCGCCTTCGCCATCCTG  CCCCATCCACTAGTGCGCCCCCGCCCCG
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (365) (401) (411) (441) (399) (393)	CG  CG  CG  CG  401  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT CGCCGCCCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCGCCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  441  480  CCCCATCCACTAGTGCGCCCCGCCGCCTTCGCCATCCTG  CCCCATCCACTAGTGCGCCCCCGCCGCCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCGCCGCCTTCCCCATCCTG  CCCCATCCACTACTGCGCCCCCGCCGCCTTCCCCATCCTG  CCCCATCCACTACTGCGCCCCCGCCGCCCTTCCCCATCCTG  CCCCATCCACTACTGCGCCCCCCGCCGCCTTCCCCATCCTG  CCCCATCCACTACTGCGCCCCCGCCGCCCTTCCCCATCCTG  CCCCATCCACTACTGCGCCCCCGCCGCCCTTCCCCATCCTG  CCCCATCCACTACTGCGCCCCCCGCCGCCTTCCCCATCCTG  CCCCATCCACTACTGCGCCCCCCGCCGCCTTCCCCATCCTG
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ala204 Val120-Ile201B	(357) (357) (357) (359) (361) (371) (401) (359) (359) (359) (365) (401) (411) (441) (399) (393) (399)	CG  401  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  CCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  CCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT  441  480  CCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCCGCGGCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCCGCGCCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCCGCGCCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCCCGCGCCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCCCGCGCCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCCCCGCGCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCCCCCGCGCTTCGCCATCCTG  CCCCATCCACTACTGCGCCCCCCCCCC
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201 Val120-Ile201 Val120-Ile201	(357) (357) (357) (359) (361) (371) (401) (359) (359) (359) (365) (401) (411) (441) (399) (393) (399) (399)	CG  401  TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT CCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT GCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT TGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT ATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCAT CCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTG CCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTG CCCATCCACTACTGCGCCCCCGCGGCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCGCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG CCCCATCCACTACTGCGCCCCCCGCCGCCTTCGCCATCCTG
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201 Val120-Ile201 Val120-Ile201 Val120-Thr202 Lys121-Val200	(357) (357) (357) (359) (361) (371) (401) (359) (359) (365) (401) (411) (441) (399) (393) (399) (399) (405)	CCCATCCACTACTGCGCCCCGGCGCGCTTCGCCATCCTG
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201 Val120-Ile201 Val120-Ile201	(357) (357) (357) (359) (361) (371) (401) (359) (359) (359) (365) (401) (411) (441) (399) (393) (399) (399)	CCCCATCCACTACTGCGCCCCGGCGCGTTCGCCATCCTGCCCCATCCAT
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201 Val120-Ile201 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus	(357) (357) (357) (359) (361) (371) (401) (359) (359) (365) (401) (411) (441) (399) (393) (399) (399) (405) (441)	CCCATCCACTACTGCGCCCCGGCGTTCGCCATCCTGCCCATCCAT
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201 Val120-Ile201 Val120-Ile201 Val120-Ile201 Val120-Ile201 Consensus  Leu122-Ser199	(357) (357) (357) (359) (361) (371) (401) (359) (357) (359) (365) (401) (411) (441) (399) (393) (399) (399) (405) (441)	CCCATCCACTACTGCGCCCCGGCGCTTCGCCATCCTGCCCATCCAT
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201C Consensus  Leu122-Ser199 Val127-Asn195	(357) (357) (357) (359) (361) (371) (401) (359) (359) (359) (365) (401) (411) (441) (399) (393) (399) (399) (405) (441)	CCCATCCACTACTGCGCCCCGGCGCTTCGCCATCCTGCCCATCCAT
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201 Val120-Ile201 Val120-Ile201 Val120-Ile201 Val120-Ile201 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B	(357) (357) (357) (359) (361) (371) (401) (359) (359) (359) (365) (401) (411) (441) (399) (393) (399) (405) (441) (451) (481) (481) (439)	CCCATCCACTACTGCGCCCCGGCGCTTCGCCATCCTGCCCCTCCCATCCAT
Val120-Ala204 Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201 Val120-Thr202 Lys121-Val200 Consensus  Leu122-Ser199 Val127-Asn195 Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201B Val120-Ile201C Consensus  Leu122-Ser199 Val127-Asn195	(357) (357) (357) (359) (361) (371) (401) (359) (359) (359) (365) (401) (411) (441) (399) (393) (399) (399) (405) (441)	CCCATCCACTACTGCGCCCCGGCGCTTCGCCATCCTGCCCATCCAT

		/ / UJ
Val120-Thr202	(439)	AAGTGCAACGACAAGAAGTTCAACGGCAGCGCCCCTGCA
Lys121-Val200	(445)	AAGTGCAACGACAAGAAGTTCAACGGCAGCGCCCCTGCA
Consensus	(481)	AAGTGCAACGACAAGAAGTTCAACGGCAGCGGCCCCTGCA
		521
Leu122-Ser199	(491)	CCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCCC
Val127-Asn195	(521)	CCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCCC
Val120-Ile201B	(479)	CCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCCC
Val120-Ala204	(473)	CCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCCC
Val120-Ile201	(479)	CONTROL CACCATGCAGTGCACCCACGGCATCCGCCC
Val120-Thr202	(479)	CCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCCC
Lys121-Va1200	(485)	CCARCGTGAGCACCGTGCAGTGCACCCACGCATCCGCCC
Consensus	(521)	CCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCCC
00.100.100		561
Leu122-Ser199	(531)	CGTGGTGAGCACCCAGCTGCTGAACGGCAGCCTGGCC
Val127-Asn195	(561)	CCTCCTCACCACCAGCTGCTGCTGAACGGCAGCCTGGCC
Val120-Ile201B	(519)	CGTGGTGAGCACCCAGCTGCTGGTGAACGGCAGCCTGGCC
Val120-Ala204	(513)	CCTCCTCACCACCCAGCTGCTGCTGAACGGCAGCCTGGCC
Val120-Ile201	(519)	CCTCCTCACCACCCACCTGCTGCTGAACGCCAGCCTGGCC
Val120 Thr202	(519)	CCTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCC
Lys121-Val200	(525)	CCTCCTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCC
Consensus	(561)	CGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCC
00	•	601
Leu122-Ser199	(571)	GAGGAGGGGTGGTGATCCGCAGCGAGAACTTCACCGACA
Val127-Asn195	(601)	GAGGAGGCGTGGTGATCCGCAGCGAGAACTTCACCGACA
Val120-Ile201B	(559)	GAGGAGGCCTGGTGATCCGCAGGGAGAACTTCACCGACA
Val120-Ala204	(553)	ENGGAGGGCGTGGTGATCCGCAGCGAGAACTTCACCGACA
Val120-Ile201	(559)	CACCACCCCTGGTGATCCGCAGCGAGACTTCACCGACA
Val120-Thr202	(559)	GAGGAGGGGTGGTGATCCGCAGCGAGAACTTCACCGACA
Lys121-Val200	(565)	GAGGAGGGCGTGGTGATCCGCAGEGAGAACTTCACCGACA
Consensus	(601)	GAGGAGGCGTGGTGATCCGCAGCGAGAACTTCACCGACA 680
		641
Leu122-Ser199	(611)	ACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGA
Val127-Asn195	(641)	ACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGGGTGGA
Vall20-Ile201B	(599)	ACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGA
Val120-Ala204	(593)	ACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGA
Val120-Ile201	(599)	ACGCCAAGACCATCATCGTCCACGTCAAGGAGAGAGCGTGGA
Val120-Thr202	(599)	ACGCCAAGACCATCATCGTGCAECTGAAGGAGAGCGTGGA
Lys121-Va1200	(605)	ACGCCAAGACCATCATCGTGCAGGTGAAGGAGAGGGTGGA
Consensus	(641)	ACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGA 720
		681 GATCAACTECACEGGCGCAACAACAACAGCCGCAAGAGC
Leu122-Ser199	(651)	GATCAACTICACCGCCCCAACAACAACAACACCCGCAAGAGC
Val127-Asn195	(681)	GATCAACTGCACCCGCCCAAGACAACAACACCCGCAAGAGC
Val120-Ile201B	(639)	GATCAACTGCACCCGCCCCAACAACAACAACACCGCAAGAGC
Val120-Ala204	(633)	GATCAACTGEACCCGCCCGAACAACAACAACACCCGCAAGAGC
Val120-Ile2 <b>01</b>	(639)	GATCAACTECACCEGCCCAACAACAACACCCGCAAGAGC
Val120-Thr202	(639)	GATCAACTGCACCCCCCCCAACAACAACAACCCCCCCAAGAGC
Lys121-Val200	(645)	GATCAACTGCACCCGCCCCAACAACAACACCCGCAAGAGC
Consensus	(681)	
		721 ATCACCATCGGCCCGGCGCGCCCTTCTACGCCACCGGG
Leu122-Ser199	(691)	ATCACCATCGGCCCGGCCGCCCTTCTACGCCACCGGCG
Val127-Asn195	(721)	
Val120-Ile201B	(679)	**************************************
Val120-Ala204	(673)	ニニー・ニー・ニー・ニー・ニー・ニー・ニー・ニー・ニー・ニー・ニー・ニー・ニー・
Val120-Ile201	(679)	
Val120-Thr202	(679)	
Lys121-Val200	(685)	
Consensus	(721)	WICHCONICORCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO

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		761 800
Leu122-Ser199	(731)	ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
Val127-Asn195	(761)	ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
	(719)	ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
Val120-Ile201B	(713)	ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
Val120-Ala204		ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
Val120-Ile201	(719)	ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
Val120-Thr202	(719)	ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
Lys121-Va1200	(725)	ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
Consensus	(761)	ACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAG
		801
Leu122-Ser199	(771)	CGGCGAGAAGTGGAACACACCCTGAAGCAGATCGTGACC
Val127-Asn195	(801)	CGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACC
Val120-Ile201B		CGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACC
Val120 1102012	(753)	CGGCGAGAAGTGGAACACACCCTGAAGCAGATCGTGACC
Val120-A1a204	(759)	CGGCGAGAAGTGGAACACACCCTGAAGCAGATCGTGACC
	(759)	CGGCGAGAAGTGGAACACACCCTGAAGCAGATCGTGACC
Val120-Thr202		CGGCGAGAACTGGAACAACACCCTGAAGCAGATCGTGACC
Lys121-Va1200	(765)	CGGCGAGAAGTGGAACACACCCTGAAGCAGATCGTGACC
Consensus	(801)	000
		041 .
Leu122-Ser199	(811)	AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCA
Val127-Asn195	(841)	AAGCTGCAGGCCAGTTCGGCAACAAGACCATCGTGTTCA
Val120-Ile201B	(799)	AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCA
Val120-Ala204	(793)	AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCA
Val120-Ile201	(799)	AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCA
Val120-Thr202	(799)	AAGCTGCAGGCCCAGTTCCGCAACAAGACCATCGTGTTCA
Lys121-Val200	(805)	AAGCTGCAGGCCCAGTTCGGGAACAAGACCATCGTGTTCA
Consensus	(841)	AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCA
Consensus	(0.1-7	881 · 920
Leu122-Ser199	(851)	AGCAGAGCAGCGGGGGGCGACCCGGAGATCGTGATGCACAG
	(881)	ACCAGACCAGCGGGGGGGCCCCGAGATCGTGATGCACAG
Val127-Asn195	(839)	AGCAGAGCAGCGGGGGGGCCCCGAGATCGTGATGCACAG
Val120-Ile201B		AGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAG
Val120-Ala204	(833)	AGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAG
Val120-Ile201	(839)	AGCAGAGCAGCGGCGGCGACCCGGAGATCGTGATGCACAG
Val120-Thr202	(839)	AGCAGAGCAGCAGCACACACACACACACACACACACACA
Lys121-Va1200	(845)	AGCAGAGCAGCGGGGGGGGCCCCGAGATCGTGATGCACAG
Consensus	(881)	AGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAG
•		
Leu122-Ser199	(891)	CTTCAACTGCGGCGGGGGAGTTCTTCTACTGCAACAGCACC
Val127-Asn195	(921)	CTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACC
Val120-Ile201B	(879)	CTTCAACTGCGGGGGGGGAGTTCTTCTACTGCAACAGCACC
Val120-Ala204	(873)	ETTERACTE CECEGE CECEGE CACTE CTACTE CAACACACAC
Val120-Ile201	(879)	CTTCAACTGCGGCGGGGGGTTCTTCTACTGCAACAGCACC
Val120 Thr202	(879)	CTTCAACTGCGGGGGGGGGTTCTTCTACTGCAACAGCACC
	(885)	CTTCAACTGCGCCGCGAGTTCTTCTACTGCAACAGCACC
Lys121-Val200	(921)	CTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACC
Consensus	(321)	961 1000
		CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCA
Leu122-Ser199	(931)	CAGCTGTTCAACAGCACCTGGAACACCATCGGCCCCA
Val127-Asn195	(961)	CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCA
Vall20-Ile201B	(919)	CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCA
Val120-Ala204	(913)	CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCA
Val120-Ile201	(919)	CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCA
Val120-Thr202	(919)	CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCA
Lys121-Val200	(925)	CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCA
Consensus	(961)	CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCA
00,,00,,00	• • •	1001
Leu122-Ser199	(971)	ACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAA
Val127-Asn195	(1001)	ACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAA
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(959) ACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAA
Val120-Ile201E
                 (953) ACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAA
Val120-Ala204
                 (959) ACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAA
 Val120-Ile201
                 (959) ACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAA
 Val120-Thr202
                 (965) ACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAA
 Lys121-Val200
                (1001) ACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAA
     Consensus
                (1011) GCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATG
 Leu122-Ser199
                (1041) GCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATG
 Val127-Asn195
                 (999) GCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATG.
Vall20-Ile201B
                 (993) GCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATG
 Val120-Ala204
                 (999) GCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATG
 Val120-Ile201
                 (999) GCAGATCATCAACCGCTGGCAGGAGGTGGGCCAAGGCCATG
 Val120-Thr202
                (1005) GCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATG
 Lys121-Val200
                (1041) GCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATG
     Consensus
                                                            1120
                       1081
                (1051) TACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCA
 Leu122-Ser199
                (1081) TACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCA
 Val127-Asn195
                (1039) TACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCA
Val120-Ile201B
                (1033) TACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCA
 Val120-Ala204
                (1039) TACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCA
 Val120-Ile201
                (1039) TACGECCCCCCATCCGEGGCCAGATCCGCTGCAGCAGCA
 Val120-Thr202
                (1045) TACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCA
 Lys121-Val200
                (1081) TACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCA
     Consensus
                (1091) ACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGGA
 Leu122-Ser199
                (1121) ACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGGA
 Val127-Asn195
                (1079) ACATCACCGGCCTGCTGCTGACCCGGGACGGCGGCAAGGA
Val120-Ile201B
                (1073) ACATCACCGGCCTGGTGGTGACCGGCGACGGCGGCAAGGA
 Val120-Ala204
                (1079) ACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGGA
 Val120-Ile201
                       ACATCACCGGCCTGCTGCTGACCCGGGACGGCGCCAAGGA
 Val120-Thr202
                (1079)
                (1085) ACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGGA
 Lvs121-Val200
                (1121) ACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGGA
     Consensus
                (1131) GATCAGCAACACCAGCGAGATCTTCCGCCCCGGCGGCGGCGGC
 Leu122-Ser199
                (1161) GATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGCCCC
 Val127-Asn195
                (1119) GATGAGCAACAGCACCGAGATCTTCCGCCCCGGCGGCGGC
Val120-Ile201B
                (1113) GATCAGCAACACEACCGAGATCTTCCGGCCCGGCGGCGGC
 Val120-Ala204
                (1119) GATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGCC
 Val120-Ile201
                       GATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGC
                (1119)
 Val120-Thr202
                (1125) GATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGCC
 Lys121-Val200
                (1161) GATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGC
     Consensus
                       1201
                (1171) GACATGCGCGAGAACTGGCGCAGCGAGCTGTACAAGTACA
 Leu122-Ser199
                      GACATGCGCGACAACTGGCGCGCGGGCGAGCTGTACAAGTACA
 Val127-Asn195
                (1201)
                (1159) GACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACA
Val120-Ile201B
                (1153) GACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACA
 Val120-Ala204
                (1159) GACATGCGCGACAACTGGCGCGCGAGCTGTACAAGTACA
 Val120-Ile201
                (1159) GACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACA
 Val120-Thr202
                (1165) GACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACA
 Lys121-Val200
                (1201) GACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACA
     Consensus
                (1211) AGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAA
 Leu122-Ser199
               (1241) AGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAA
 Val127-Asn195
                (1199) AGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAA
Val120-Ile201B
                (1193) AGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAA
Val120-Ala204
                (1199) AGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAA
 Val120-Ile201
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Consensus

		1560
	(1401)	1521 CCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Leu122-Ser199	(1491)	GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Val127-Asn195	(1521)	GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Val120-Ile201B	(1479)	GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Val120-Ala204	(1473)	GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Val120-Ile201	(1479)	GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Val120-Thr202	(1479)	GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Lys121-Val200	(1485)	GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Consensus	(1521)	GCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG
Leu122-Ser199	(1531)	GGCATCTGGGGCTGCAGCGGCAGCTGATCTGCACCACCG
Vall27-Asn195	(1561)	GGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCG
Val120-Ile201B	(1519)	GGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCG
Val120-Ala204	(1513)	GGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCG
Val120-Ile201	(1519)	GGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCG
Val120-Thr202	(1519)	GGCATCTGGGGCTGCAGCGGCAAGGTGATCTGCACCACCG
Lys121-Va1200	(1525)	GGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCG
Consensus	(1561)	GGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCG
		1601 1640
Leu122-Ser199	(1571)	CCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
Val127-Asn195	(1601)	CCGTGCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
Val120-Ile201B	(1559)	CCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
Val120-Ala204	(1553)	CCGTGCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
Val120-Ile201	(1559)	CCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
Val120-Thr202	(1559)	CCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
Lys121-Val200	(1565)	CCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
Consensus	(1601)	CCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA
		1641
Leu122-Ser199	(1611)	CCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGC
Val127-Asn195	(1641)	CCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGC
Val120-Ile201B	(1599)	CCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGC
Val120-Ala204	(1593)	CCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGC
Val120-Ile201	(1599)	CCACATCTGGAAGAACATGACCTGGATGGAGTGGGAGGGC
Val120-Thr202	(1599)	CCAGATCTGGAACAACATGACCTGGATGGAGTGGAGCGC
Lys121-Val200	(1605)	CCAGATCIGGAACAACATGACCIGGATGGATGGGAGCGC
Consensus	(1641)	CCAGATCTGGAACAACATGACCTGGATGGAGTGGAGCGC
		1001
Leu122-Ser199	(1651)	GAGATCGACAACTACACCAACCTGATCTACACCCTGATCG
Val127-Asn195	(1681)	GAGATEGACATETACACCAACCTGATETACACCCTGATCG
Val120-Ile201B	(1639)	GAGATEGACAACTACACCAACCTGATCTACACCCTGATCG
Val120-Ala204	(1633)	GAGATEGACAACTACACCAACCTCATCC
Val120-Ile201	(1639)	GAGATEGACAACTACACCAACCTGATCTACACCCTGATCG
Val120-Thr202	(1639)	GAGATEGACAACTACACEAAGCTEATETACACCCTGATEG
Lys121-Val200	(1645)	GAGATCGACAACTACACCAACCTGATCG
Consensus	(1681)	GAGATCGACAACTACACCAACCTGATCTACACCCTGATCG
		1721
Leu122-Ser199	(1691)	AGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCT
Val127-Asn195	(1721)	AGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCT
Val120-Ile201B	(1679)	AGGAGAGCCAGAACCAGCAGGAGAACGAGCAGCAGCAGCA
Val120-Ala204	(1673)	AGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCT
Val120-Ile201	(1679)	AGGAGAGCCAGAACCAGCAGGAGCAGCAGCAGCAGCAGCA
Val120-Thr202	(1679)	AGGAGAGCCAGAACCAGCAGGAGGAGCAGCAGCAGCAGCA
Lys121-Val200	(1685)	AGGAGAGCCAGAACCAGCAGGAGCAGCAGGAGCT
Consensus	(1721)	AGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCT
*		
Leu122-Ser199	(1731)	GCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTC
Val127-Asn195	(1761)	GCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTC

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(1719) GCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTC
 Val120-Ile201B
  Val120-Ala204
                  (1713) GCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTC
                  (1719) GCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTC
  Val120-Ile20i
  Val120-Thr202
                  (1719) GCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTC
  Lys121-Va1200
                  (1725) GCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTC
      Consensus
                  (1761) GCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTC
                                                             1840
  Leul22-Ser199
                  (1771) GACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCA
  Val127-Asn195
                  (1801) GACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCA
 Val120-Ile201B
                  (1759) GACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCA
  Val120-Ala204
                        GACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCA
                  (1753)
  Val120-Ile201
                  (1759)
                        GACATCAGCAAGTGGCTGTGGTAGATCAAGATCTTCATCA
  Val120-Thr202
                 (1759) GACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCA
  Lys121-Val200
                 (1765) GACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCA
                 (1801) GACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCA
      Consensus
 Leu122-Ser199
                 (1811) TGATCGTGGGGGGCCTGGTGGGCCTGCGCATCGTGTTCAC
 Val127-Asn195
                 (1841)
                        TGATCGTGGGCGGCCTGGTGGGCCTGCGCATCGTGTTCAC
 Val120-Ile201B
                        TGATEGTGGGCGGCCTGGTGGGCCTGCGCATCGTGTTCAC
                 (1799)
 Val120-Ala204
                 (1793)
                        TGATCGTGGGCGCCTGGTGGGCCTGCGCATCGTGTTCAC
 Val120-Ile201
                 (1799)
                        TGATCGTGGGCGGCCTGGTGGGCCTGCGCATCGTGTTCAC
 Val120-Thr202
                 (1799)
                        TGATCGTGGGGGGCCTGGGGCCTGCGCATCGTGTTCAC
 Lys121-Val200
                 (1805)
                        TGATEGTGGGCGCCTGGTGGGCCTGCGCATCGTGTTCAC
     Consensus
                 (1841) TGATCGTGGGCGGCCTGGTGGGCCTGCGCATCGTGTTCAC
                 (1851) CGTGCTGAGCATCGTGAACCGGGTGCGCCAGGGCTACAGC
 Leu122-Ser199
                 (1881) CGTGCTGAGGATCGTGAACCGCGTGCGCCAGGGCTACAGC
 Val127-Asn195
Vall20-Ile201B
                        CGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGC
                        CGTCCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGC
 Val120-Ala204
                 (1833)
 Val120-Ile201
                 (1839) CGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGC
 Val120-Thr202
                 (1839) CGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGC
 Lys121-Va1200
                 (1845) CGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGC
     Consensus
                 (1881) CGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGC
                 (1891) ECCCTGAGOTTICCAGACCGCOTTICGECGCCCCCCGCGGGGCC
 Leul22-Ser199
                 (1921) CCCCTGAGETTECAGAGEGGGGTTTGGCGGGCCCCGGGGGCC
 Val127-Asn195
Val120-Ile201B
                (1879)
                       decentracentecagaececentrecescecececececece
 Val120-Ala204
                (1873)
                       eccongaceurceagacececonvecescececececece
 Val120-Ile201
                (1879)
                       CCCCTGAGCTTCGAGACCCGCGCTTTCGCCGCCCCCCCGCGGGC
 Val120-Thr202
                (1879) CCCCTGAGCTTCCAGACCCGCTTCCCGCGCCCCCGCGGCCC
 Lys121-Val200
                (1885) CCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCCGCGGCC
     Consensus
                (1921) CCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCCGCGGCCC
                       1961
                                                            2000
 Leu122-Ser199
                (1931) CEGACCGCCCGAGGGCATTCGAGGAGGAGGGGGGGGGGAGCG
 Val127-Asn195
                (1961)
                       Degacegegegeaggeannefageaggagggcggggaggg
                       <u>CCCACCCCCCCCAGGGCATCGAGGAGGAGGGCGCGAGCG</u>
Val120-Ile201B
                (1919)
 Val120-Ala204
                (1913)
                       ECGACCGECECGAGGGCATCGAGGAGGAGGGCGGCGAGCG
 Val120-Ile201
                (1919)
                       CCGACCGCCCGAGGCATCGAGGAGGAGGGCGCGAGCG
 Val120-Thr202
                (1919)
                       CCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGCGCGAGCG
 Lys121-Val200
                (1961) CCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCG
     Consensus
                (1971) CGACCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTG
Leu122-Ser199
                (2001) CGACCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTG
 Val127-Asn195
                (1959) CGACCGCGACCGCAGCAGCCCCTGGTGCACGGCCTGCTG
Val120-Ile201B
Val120-Ala204
                (1953) CGACCGCGACCGCAGCAGCCCCTGGTGCACGGCCTGCTG
 Val120-Ile201
                (1959) CGACCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTG
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(1959) CGACCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTG
 Val120-Thr202
                 (1965) CGACCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTG
 Lvs121-Val200
                 (2001) CGACCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTG
     Consensus
                (2011) GCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCA
 Leu122-Ser199
                (2041) GCCCTGATCTGGGAGGACCTGCGGAGCCTGTGCCTGTTCA
 Val127-Asn195
                 (1999) GCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCA
Val120-Ile201B
                 (1993) GCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCA
 Val120-Ala204
                (1999) GCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCA
 Val120-Ile201
                (1999) GCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCA
 Val120-Thr202
                (2005) GCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCA
 Lys121-Val200
                (2041) GCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCA
     Consensus
                                                           2120
                       2081
                (2051) GCTACCACCGCCTGCGCGACCTGATCGCCGCCCG
 Leu122-Ser199
                (2081) GCTACGACGGCCTGCGGGGCCTGATCCTGATCGCCGCCGG
 Val127-Asn195
                (2039) GCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCGG
Val120-Ile201B
                (2033) GCTACCACCGCCTGCGCGACCTGATCCTGATCGCCCCCCG
 Val120-Ala204
                (2039) GCTACCACCGCCTGCGCGAGCTGATCCTGATCGCCGCCGG
 Val120-Ile201
                (2039) GCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCCG
 Val120-Thr202
                (2045) GCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCGG
 Lys121-Val200
                (2081) GCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCCG
     Consensus
                       2121
                (2091) CATEGTGGAGCTGCTGGGCCGCGGGGGGGGGGCCCTG
 Leu122-Ser199
                (2121) GATGGTGGAGCTGCTGGGCCGCGCGGGGTGGGAGGCCCTG
 Val127-Asn195
                       Val120-Ile201B
                (2079)
                       CATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGGCCCTG
 Val120-Ala204
                (2073)
                (2079) CATCGTGGAGCTGCTGGGCCGCGGGGTGGGAGGCCCTG
 Val120-Ile201
                (2079) CATCGTGGAGCTGCTGGGCCGCGCGGCTGGGAGGCCCTG
 Val120-Thr202
                (2085) CATCGTGGAGCTGCTGGGCCGCCGCGGGGGGCCCTG
 Lys121-Val200
                (2121) CATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGGCCCTG
     Consensus
                (2131) ANGINGTEGECCANCETEGEGEACTACTEGATCCAGGAGC
 Leu122-Ser199
                (2161) AAGTACTGGGGGAAGCTGCTGCAGTACTGGATCCAGGAGC
 Val127-Asn195
                (2119) AAGTACTGGGGCARCCTGCTGCACTACTGGATCCAGGAGC
Val120-Ile201B
                (2113) AAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGC
 Val120-Ala204
                (2119) AAGTACTGGGGGAACGTGGTGGAGTACTGGATGCAGGAGC
 Val120-Ile201
                      NAGTACTGGGGCAACCTCCTGCACTACTGGATCCAGGAGC
                (2119)
 Val120-Thr202
                      AAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGC
 Lys121-Val200
                (2125)
                (2161) AAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGC
     Consensus
                                                           2240
                (2171) TGAAGAACAGGGCCGTGAGCCTGTTCGACGCCATCGCCAT
 Leu122-Ser199
                      tgaagaacagegegegegegegegegecategecat
                (2201)
 Val127-Asn195
                      TENAGNAGACGGGGGGGAGCGACGTCATFXGGAGCGGAATGGCCAT
Val120-11e201B
                      TGAAGAACAGEGEGETGAGEETETEGEACGECATEGCCAT
 Val120-Ala204
                      TGAAGAACAGGGCCCTGAGGETGTTCGACGCCATCGCCAT
                (2159)
 Val120-Ile201
                      TIGATGATEAGEGETEAGEGTETETEGAGGCATCGCCAT
                (2159)
Val120-Thr202
                (2165) TGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCAT
 Lys121-Val200
                (2201) TGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCAT
     Consensus
                       2241
                (2211) CGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCC
 Leu122-Ser199
                (2241) CGCCGTGGCCGAGGGCACCGCATCATCGAGGTGGCC
 Val127-Asn195
                (2199) CGCCETGGCCGAGGGGACCGACCGCATCATCGAGGTGGCC
Val120-Ile201B
                (2193) CGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCC
 Val120-Ala204
                (2199) CGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCC
 Val120-Ile201
                (2199) CGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCC
Val120-Thr202
                (2205) CGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCC
 Lys121-Val200
               (2241) CGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCC
    Consensus
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			2320
		2281	
Leu122-Ser199	(2251)	CAGCGCATCGGCCGCGCCTTCCTGC	ACATCCCCCGCCGCA
Val127-Asn195	(2281)	CAGCGCATCGGCCGCGCCTTCCTGC	ACATECCCCGCGGCA
Vall20-Ile201B	(2239)	CAGCGCATCGGCGGGGCCTTCCTGG	ACATECECEGECGEA
Val120-Ala204	(2233)	CAGCGCATCGGCGCGCGTTCCTGC	ACATCCCCCGCGGA
Val120-Ile201	(2239)	CAGCGCATCGGCCGCGCCTTCCTGC	ACATECECCGCCGCA
Val120-Thr202	(2239)	CAGCGCATCGGCCGCGCCTTCCTGC	ACATCCCCCGCCGCA
Lys121-Va1200	(2245)	CAGCGCATCGGCCGCGCCTTCCTGC	ACATCCCCCGCCGCA
Consensus	(2281)	CAGCGCATCGGCCGCGCCTTCCTGC	
		2321	2360
Leu122-Ser199	(2291)	TCCCCCAGGGCTTCCAGGGGGCCCCI	GCTGTAACTCGA <b>GC</b> G
Val127-Asn195	(2321)	TCCGCCAGGGCTTCGAGCGCGCCCT	GCTGTAACTCG <b>AG</b>
Val120-Ile201B	(2279)	TCCGCCAGGGCTTCGAGGGGGCCCT	GETGTAACTCGAGCG
Val120-Ala204	(2273)	TCCGCCAGGCCTTCGAGCGCGCCCI	GCTGTAACTCG <b>AG</b>
Val120-Ile201	(2279)	TCCCCCAGGCCTTCGAGCCCCCC	GCIGTAACTCG <b>AG</b>
Val120-Thr202	(2279)	TCCGCCAGGGCTTCGAGGGGGCCCC	GCTGTAACTCG <b>AG</b>
Lys121-Val200	(2285)	TCCGCCAGGGCTTCGAGCGCGCCCT	GCTGTAACTCGA <b>GC</b> G
Consensus	(2321)	TCCGCCAGGGCTTCGAGCGCGCCCT	GCTGTAACTCGAG
		2361	
Leu122-Ser199	(2331)	TGCT	
Val127-Asn195	(2359)		
Val120-Ile201B	(2319)	TGCT	
Val120-Ala204	(2311)		
Val120-Ile201	(2317)		
Val120-Thr202	(2317)		•
Lys121-Val200	(2325)	TGCT	
Consensus	(2361)		

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		10 / 03
Trp427-Gly431	(201)	ब्रोसेट्राः गर्भात्रे संस्थाने विद्याने हे स्ट्राह्म स्ट्राह्म स्ट्राह्म स्ट्राह्म स्ट्राह्म स्ट्राह्म स्ट्राह
Gln422-Tyr435B	(201)	वस्तान्त्र तत्तानास्य वस्तानास्य वस्तानास्य वस्तानात्त्र वस्तानात्त्र वस्तानात्त्र वस्तानात्त्र वस्तानात्त्र व
Arg426-Gly431	(201)	द्रसम्दर्भकारकप्रदानव्यक्तरकारम्बद्रस्थितम्।
Ile423-Met434	(201)	Beleviorie totale addiction of the transfer of the contraction of the
Gln422-Tyr435	(201)	वस्तराभ्यकाराभवविष्याभ्यविष्यभ्यकाराज्ञात्रभ्यताक्ष्यकार्
Arg426-Lys432	(201)	સંદોલામાં માત્ર જ પ્રવાસ કરાયા છે. તે કે માત્ર કર્યા છે. તે તે માત્ર કર્યા છે. તે કે માત્ર કર્યા છે. તે માત્ર ક
Arg426-Gly431B	(201)	adeloved Matricka longeration aspersant valence
Asn425-Lys432	(201)	संस्थितिक प्रतास्त्र विश्वकारम् । अस्ति । १००० विश्वकारम् । १००० विश्वकारम्
Consensus	(201)	GGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAG
Consensus	(201)	241 280
Ile424-Ala433	(241)	evernacing englavation and residuations in a top to t
Trp427-Gly431	(241)	HARINGE PROPERTY AND CONTRACTOR AND AND CONTRACTOR AND AND CONTRACTOR AND CONTRAC
		GVANTECASE CASCULATION CONTRACTOR
Gln422-Tyr435B	(241)	
Arg426-Gly431	(241)	witchneterremetalitatitementerioritation
Ile423-Met434	(241)	ENGRANGING NEGARANAGENCIAN GENERALING SERVING
Gln422-Tyr435	(241)	Bitainne encantedalle ayelenatie elettanica hantainne han
Arg426-Lys432	(241)	ले प्रयोगालक प्रवेत प्रयोग
Arg426-Gly431B	(241)	enterminente enterminente interminente inter
Asn425-Lys432	(241)	ETENNECHE SEGVOTATE EN GIVER CONTENTATE MENTER MANTE
Consensus	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGT
		281 320
Ile424-Ala433	(281)	adianaminaminess develores social ediciensianess
Trp427-Gly431	(281)	elutytinitatoitateaucionasitatoistiteita etototatainoitatoita
Gln422-Tyr435B	(281)	्टोक्रोक्षक्रमण्डकालः आद्दित्।।वाद्यात्रक्षम् वर्षाद्यक्रमण्डकार्थकारम् वर्षा
Arg426-Gly431	(281)	e, a y sta i? Ye. sefes sejes sejes fent fent fan een as (a flejen fen near en) f
Ile423-Met <b>434</b>	(281)	ktara/divides are pricining and entranted medicing and entrances from the
Gln422-Tyr4 <b>3</b> 5	(281)	datalalalatatakonnedingateatattatteateateatattatt
Arg426-Lys4 <b>32</b>	(281)	devyen wenne y retardeviden en retangualde over jern
Arg426-Gly431B	(281)	ggragator:@angerchage.chagachtgardardard
Asn425-Lys432	(281)	GENNICAND UNICATEGRICAN SERVICIONE GALCANICAN
Consensus	(281)	GGAAGAACATGGTGGAGCAGATGCACGAGGACATCAT
		321 360
Ile424-Ala433	(321)	with the characteristic transfer on control in prediction in the
Trp427-Gly431	(321)	wider and conferred traffic inscrinities of a conferred in
Gln422-Tyr435B	(321)	<ul><li>अस् अस्तर्भस्तरस्योषः अत्रव्यविष्यः स्तित्रप्रतः १,० १ स्वरः विषयः द्विषयः</li></ul>
Arg426-Gly431	(321)	agecjeski, kajaletije išarstilje ospetaritacion seoje stotritate se
Ile423-Met434	(321)	AVECTOR CONTROL OF AN AVECTOR OF A CONTROL CONTRACTOR OF A CON
Gln422-Tyr435	(321)	रत्यवाद्यां सामग्रहस्य विवस्ति । अस्ति
Arg426-Lys432	(321)	egite elenferget eletategitative posterative elejen eletategitation eta trefant e
Arg426-Gly431B	(321)	कर्पसालाभूकरः इतिस्थारकातम् (स्थापना १०५५) । । । । । । । । । । । । । । । । । ।
Asn425-Lys4 <b>32</b>	(321)	WASCLING NO HOLD SELVE VENE WON VOICE CHESC SELVE COLLYCTION
Consensus	(321)	CAGCCTGTGGGACCAGAGCCTGAAGCCTGCGTGAAGCTG
		361 400
Ile424-Ala433	(361)	ત્રવાલનાના લામ લામ લામ લામ લામ કારણ છે. જે તેમ જ જો લામ લામ લામ કરવા છે. જે જો છે. જે જો છે. જે જો છે. જે જો છ
Trp427-Gly431	(361)	More of classical explanations of executive executive executive expression (25%) ex-
Gln422-Tyr435B	(361)	Welching condition of the condition of the state of the sayour
Arg426-Gly431	(361)	Helencharten ette megnetar kolt nyertur melopt metaning nyelytter.
Ile423-Met434	(361)	iteles er et en met en neuen en en ment en neuen en e
Gln422-Tyr435	(361)	TO CONTROL CONTROL SEMENTIAL CONTROL SENTING
Arg426-Lys <b>432</b>	(361)	Totaleste mention entermette intermeter (entermeter)
Arg426-Gly431B	(361)	Heriographer have entergrapher by the teacher of the property
Asn425-Lys432	(361)	Reduccionalica en en en en estace de la composição de la
Consensus	(361)	ACCCCCTGTGCGTGACCCTGCACCTGCACCTGAAGA
•		401 440
Ile424-Ala433	(401)	भवन्। अत्याजा । अत्य
Trp427-Gly431	(401)	Keleinyeensestestanalidessestaanyeenskaa
Gln422-Tyr435B	(401)	Maleranimental content in a law in a manual translation in the contract of the

11 0 00/3/202		17 / 05
Arg426-Gly <b>431</b>	(401)	न्द्रियात्तानुस्त्रात्त्रम् स्वात्त्रस्य स्वात्त्रस्य स्वात्त्रस्य त्यात्त्रस्य स्वात्त्रस्य स्वात्त्रस्य स्वात
Ile423-Met <b>434</b>	(401)	Telefore, que está feli de la falle de la facto de la contrata de la falle de la facto de la falle de la falle
Gln422-Tyr <b>435</b>	(401)	<i>પેલેલ્ડિલ્સુલ્સમેડ્લેડ્સુમાલેડ્સુનલ્સાનલ્સ્ડ્રિયલેડ્સુનલ્સુના</i>
Arg426-Lys <b>432</b>	(401)	igenderestroicaina estidora has apolicitat di triscinale intracionalida interiora.
Arg426-Gly431B	(401)	મીલારારા ભાગ ભાગમાં ભાગમાં મુક્ત કર્યા છે. તેમ માના માતા છે. જે માના માના માતા માતા છે. જે માના માતા માતા માતા
Asn425-Lys <b>432</b>	(401)	sycieti essyctotivitetivicisticistessyctetis sychetesis setaticism telesis
Consensus	(401)	ACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGATGGA
		441 480
Ile424-Ala <b>43</b> 3	(441)	૱ૡૡૡૡૡ <b>ૡૺૡ</b> ૽ૠ૽ૡ૽૽ઌૻૢૡઌ૽ઌ૽ૡ૽ૡ૽ઌ૽૱ૡૡૢૡઌૹૢૡૡ૽૱ૡ૽ૡૹઌ
Trp427-Gly431	(441)	र एदि दिन्दि दिन्दि से पुर्वा रेपी कर में स्वरंग में एक में दिन में में एक में से में में एक दिन में दिन में दि
Gln422-Tyr435B	(441)	न्थर्वारायस <b>स्यान्त्रम्</b> राद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धसम्बद्धस
Arg426-Gly <b>431</b>	(441)	macromatermental and individual content of the second
Ile423-Met <b>434</b>	(441)	construction and this sales are sale indicated in the paper and called a construction and the called and called an experience and called an experi
Gln422-Tyr <b>43</b> 5	(441)	enclosed and introduced and enclosed characteristics.
Arg426-Lys <b>432</b>	(441)	eococidectrotrotrotrotrotrotrotrotrotrotrotrotrot
Arg426-Gly431B	(441)	Hatelanced factor attacks to the envariant contractions of
Asn425-Lys <b>432</b>	(441)	ार दिल्ले के प्रमाण भूमा कर्म महिला है। इस है। इस है। इस है। इस है। इस है।
Consensus	(441)	CCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACC
		481 520
Ile424-Ala <b>433</b>	(481)	१,८१८११११८८८। व्याकार १,८६१४५१८८। व्याकार हो ।
Trp427-Gly <b>431</b>	(481)	Tentification of the state of t
Gln422-Tyr435B	(481)	igatorie versielelinigation attority electrolity telestre la frequence i
Arg426-Gly <b>431</b>	(481)	neighbeit wieler is Neity Verbeiteit ein beite beite auf eine beite bing auf
Ile423-Met <b>434</b>	(481)	"thick trickers to be to the text of the trick to the trick to the text of the text.
Gln422-Tyr435	(481)	determination of the support of the state of the second
Arg426-Lys432	(481)	Tensis codestantamedestamentalestes (con of cono
Arg426-Gly431B	. (481)	the concludes a table of the estate in the season in the s
Asn425-Lys4 <b>32</b>	(481)	Action and a second second in the second in
Consens <b>us</b>	(481)	AGCATCCGCAACAAGATGCAGAAGGAGTACGCCCTGTTCT
		521 560
Ile424-Ala433	(521)	restricted the extension and the properties of t
Trp427-Gly431	(521)	Herrings relaine enteles de la entre le committe de la communité de la communité de la communité de la communi
Gln422-Tyr435B	(521)	भुवक्र के दोरु में सीराहर अने सीराहर सामानिक सामानिक कर है। इस के किया के किया है कि किया है। इस किया किया कि
Arg426-Gly431	(521)	Medit of the great representating the Section, electrics, special defendencies of the
Ile423-Met434	(521)	weaktern of elegate engelos amojos samojos atrodes y carticles (2.1,7) elegate atrodes
Gln422-Tyr435	(521)	destributes established and an antimient established and and
Arg426-Lys432	(521)	Activities and control of the contro
Arg426-Gly431B	(521)	tressages a classe can classe contract and the contract of the
Asn425-Lys432	(521)	VonVersideVerditelesses convertents in the Surge Services
Consensus	(521)	ACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAG 561 600
T1 ~ 424 - 71 - 422	15611	
Ile424-Ala433 Trp427-Gly431	(561) (561)	sanya sa sanagan sa uda agaman manua ana ang ana ana sa sa sanya matangan sa utangan sa
Gln422-Tyr435B	(561)	Salvanicio septembrita selemento en en carente en en escribir en en el como de como en el como en el como en e
Arg426-Gly431	(561)	
Ile423-Met434	(561)	saktuolistaalenyditaatastakialejastysiestydestaepatekjessa setitajakkia Partijastelenteismistrikainestyteinestyteityteistaete eriteikaaleisestytte
Gln422-Tyr435	(561)	
<del>-</del>		
Arg426-Lys432 Arg426-Gly431B	(561) (561)	
Arg426-G1y4318 Asn425-Lys432	(561)	<u>entrophological dentrophological dentro</u>
Consensus	(561)	CTACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAG
Consensus	(20T)	601 640
Ile424-Ala433	(601)	ସଙ୍ଜ୍ୟସଙ୍ଜ୍ୟପର୍ମ୍ୟପରମିୟଧସର୍ମନ୍ୟପରମଣ୍ଟ ହେଏ। ୭୦୦
Trp427-Gly431	(601)	demanderavidensavennikleviels manderavines vir
Gln422-Tyr435B	(601)	CONTROL OF THE CHANGE OF THE CONTROL
Arg426-Gly431		EGERRORIAGO PARA PARA PARA PARA PARA PARA PARA PAR
Ile423-Met434	(601)	designations are serviced by the service services of the service o
TTC-150 MECADA	(001)	

FIG. 4C

		10 / 00
Gln422-Tyr435	(601)	म्बलकाम्बलक्ष्यान्त्रभाष्ट्रविष्टम्बलक्षयान्त्रकात् । व्यवस्तर्वाद्यकाम्बलक्षयान्त्रकार्यकारः
Arg426-Lys432	(601)	efele anterferentiferation per en activité reservation de les procédes des contrations de la contration de l
Arg426-Gly431B	(601)	deconcioses pareigravelon presente econocio este presente en presente en presente en presente en presente en p
Asn425-Lys4 <b>32</b>	(601)	en-concluded with the control of the
Consensus	(601)	GCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACT
		641 680
Ile424-Ala433	(641)	प्रमास्यस्य स्वतं स्
Trp427-Gly431	(641)	<b>प्राप्तस्ते सञ्चल स्टाय स्टाय त्या त्या त्या स्टाय स्टाय होत्य स्टाय स</b>
Gln422-Tyr435B	(641)	METHOLOGOGOLOGIC SIGGIC CONTROL CONTROL CONTROL CONTROL
Arg426-Gly431	(641)	Vernantarios de designacións de entractimiento de la proprieda de la proprieda de la proprieda de la proprieda
Ile423-Met434	(641)	Herneredereren eigen ein fechnichteren ferfanzen ein fiert.
Gln422-Tyr435	(641)	Lancadescaped de la company de
Arg426-Lys432	(641)	୵୵୷୳ଢ଼ୠ୶୳୰୶ଢ଼ୠଢ଼ୠଢ଼ୠଢ଼ଽ୳୲୲୷୰ୄ୲୕୷ୢଽ୷୕ୣ୷ଊ୵ଢ଼ୢ୵ୡୡ୵୶ୠ୵ୡୠୡୠ
Arg426-Gly431B	(641)	Membeloicherenen of errene hand contract man electricity
Asn425-Lys432	(641)	୵୵୶୶ୡ୰ୠୠୠୠୠୡୡୡୡୡୡୡ୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷
Consensus	(641)	ACTGCGCCCCGCCGGCTTCGCCATCCTGAAGTGCAACGA
		681 720
Ile424-Ala433	(681)	MAYEN GERANICEEN COURTE CONTENTED TO CARRIAGE
Trp427-Gly431	(681)	#XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Gln422-Tyr435B	(681)	क्ष् <i>रत्विक्षम्</i> लाक्षरस्रितमस्रविद्यारस्तिसस्य १००४ स्त्रीलगुलस्य अस्तरस्य स्थल
Arg426-Gly431	(681)	CHANGIANTER NA GIRENAMENCICA CIRCUMATO MANAGERA MATCICA
Ile423-Met434	(681)	STATELY TO ANY STATE OF COMES, CICIO OF SUCCESSION OF THE CASE AND
Gln422-Tyr435	(681)	ANACHMANIACHARCECTONELECCONOLONIC MECANOCHMANICHCANCAC
Arg426-Lys432	(681)	wayerayeranayyadesay.coddaayastodygeayydesyyte
Arg426-Gly431B	(681)	SMALE WATCHING STATE CHESTICS CONTROL OF THE STATE OF A CONTROL OF THE STATE OF
Asn425-Lys432	(681)	environnen kenvirgelen hydrolockielen ener en wonnigen hydre
Consensus	(681)	CAAGAAGTTCAACGGCAGCGGCCCCTGCACCAACGTGAGC
		721
Ile424-Ala433.	(721)	instrates in the residence of the resident of
Trp427-Gly431	(721)	VOLUMENACO V CHRACA V RACATO CACARA CORLA RECENTORA (C. YOUR
Gln422-Tyr435B	(721)	None township with the contraction of the second contraction of
Arg426-Gly431	(721)	ACCENT CINCING OUT OF CONTROL OF THE
Ile423-Met434	(721)	Aprichatication de la contraction de la contract
Gln422-Tyr435	(721)	Versionsteller terminalistic projecter er enter eine enterprise bestalten
Arg426-Lys432	(721)	Herale sales was held well is builded to the restrict of proclain action with the te
Arg426-Gly431B	(721)	research and a property of the second
Asn425-Lys432	(721)	the elemental designation is the present the content of the conten
Consensus	(721)	ACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCA
		761 800
Ile424-Ala433	(761)	୶ଡ଼ଊ୳ଌ୕ଌ୲୲୷୰୶ୣ୵୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷
Trp427-Gly431	(761)	ल्लान्स् वर्षः हर्त्यात्रिः विद्यान्ति । विद्यान्ति । विद्यान्ति । विद्यान्ति । विद्यान्ति । विद्यान्ति । विद्य
Gln422-Tyr435B	(761)	elelettale inclusificio nettat niciestate el conficienzi el tata de la conficienza el conficienza de la conficienza del conficienza de la
Arg426-Gly431	(761)	stepater veriller hermit editateren eelikedivelerisi
Ile423-Met <b>434</b>	(761)	ale ale established and the second of the selection of th
Gln422-Tyr435	(761)	स्टाः व्हार्क्यस्य स्थापना अस्ति । स्टार्का स्थापना स्थापना । स्टार्का स्थापना स्थापना । स्थापना स्थापना । स्थ स्थापना स्थापना स्थापना स्थापना । स्थापना स्थापना स्थापना । स्थापना स्थापना स्थापना । स्थापना स्थापना स्थापना
Arg426-Lys <b>432</b>	(761)	෦෭෮෭෭෭෦ඁ෯෬෦෦ඁ෮෫෦෦෭෦෭෦෦෦෧ඁ෭෦෭෦෦෦෧෮෭෦෦෦෦෦෭෦෦෦෦෮෦෦෮෧෦෦෦෧ඁ෧ඁ෭ <mark>෦෧෧෦෦෧෧෦෦෧෧෦෦</mark> ෦
Arg426-Gly431B	(761)	Section Configuration of the c
Asn425-Lys <b>432</b>	(761)	APENCIO NECENCIONAMO CENTRE CON CONTRACO CONTRACO CONTRA
Consensus	(761)	CCCAGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGT
		801 840
Ile424-Ala433	(801)	सेक्षणकारणकारणकारणकारणकारणकारणकारणकारणकारणकार
Trp427-Gly431	(801)	gewalphsedancedvalationhjchegaltalingeogyttallog
Gln422-Tyr435B	(801)	emperationed very department of the value of
Arg426-Gly431	(801)	ਖ਼ਫ਼ਸ਼ਫ਼ਜ਼ਸ਼ਫ਼ਜ਼ਸ਼ਫ਼ਫ਼ਫ਼ਫ਼ਸ਼ਫ਼ਖ਼ਫ਼ਖ਼ਖ਼ਫ਼ਸ਼ਫ਼ਸ਼ਫ਼ਸ਼ਫ਼ਜ਼ਫ਼ਫ਼ਜ਼ਫ਼ਫ਼ਜ਼ਫ਼ਫ਼ਜ਼ਫ਼ਫ਼ਜ਼ਫ਼ਫ਼ਫ਼ਜ਼ਫ਼
Ile423-Met434	(801)	egrannegganderfaktennenteregganjeggganieveg
Gln422-Tyr435	(801)	dextalatiquestallationstrantestidatiessigatestilesor
Arg426-Lys432	(801)	बिस्मारमभन्द्रायसंग्रहाराचे गुरुष्ट्रातासम्बद्धाः । । । । । । । । । । । । । । । । । । ।

Arg426-Gly431B	(801)	वक्षायोभारतस्वकागवनसंग्रमभारतः। । । । । । । । । । । । । । । । । । ।
Asn425-Lys4 <b>32</b>	(801)	ૡ <b>ૡૡ૽</b> ૽ૠઌ <b>ૡૡૺઌ૽</b> ઌૡૺૡઌૡઌ૱ૹૹૡૡ૽ઌઌઌૡ૽૽ૡ૱ૡઌઌૡૡૡ૱ૹૡ૿ૡઌૡ
Consensus	(801)	GGTGATCCGCAGCGAGACTTCACCGACAACGCCAAGACC
		841 880
Ile424-Ala433	(841)	ः इतिर्यक्तित्। द्याप्तदावाक्ष्यं विद्यक्तिकारिया द्यार्ग्यः गत्यात् विद्यक्षित् व्यक्तिकारिया विद्यार्थिया वि
Trp427-Gly431	(841)	we med accompany calcinolance in a second contraction
Gln422-Tyr435B	(841)	INNERGREGATE REPAREMENT OF THE LOWING THE T
Arg426-Gly431	(841)	MIGNERSCHIEMVERMEN VRIEWCVICKEN (EN VIEW MED VIEW KEN V
Ile423-Met434	(841)	inkesinnolwardoinejonfeitaitofeaitoineloneeneetiekiykuiti(ehkelei)
Gln422-Tyr435	(841)	MIGNICENCENSEMBLY MEDICAGORICENS AND MENTERICEN
Arg426-Lys432	(841)	PROVINCE VEED HOURS STEED (CLARCES COVERS AND BREED)
Arg426-Gly431B	(841)	SYCHTHERS CHACK REPAYERMENT OF CHECKING A PROPERTY CHECKING A PROP
Asn425-Lys432	(841)	and interest the control of the cont
Consensus	(841)	ATCATCGTGCAGCTGAAGGAGAGCGTGGAGATCAACTGCA
		881 920
Ile424-Ala433	(881)	Sector secretic receiving the colorate with the properties of
Trp427-Gly431	(881)	ୠ <b>ୄ୷ୠ୷</b> ୰୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷
Gln422-Tyr435B	(881)	ૡ૽ૡ૽ૼૡ૿ૡૺઌઌૹઌ૽૽ઌ૽૽ૹ૽ૡઌ૽ૹઌૹઌઌૡૡ૽ૡ૽ૹૢૡઌ૽ૡ૽ૡૡઌૹ૽૽ૡ૽૽ૡ૽ૡ૽ૡ૽ૡ૽ૡૡ૽
Arg426-Gly431	(881)	GRINGARIO CATALOS AVENTA CENTRA LA CATA DE CATALOGA DE
Ile423-Met434	(881)	storienteria (@Artha reactorie) a tepten and a sangere
Gln422-Tyr435	(881)	ઋલેલદ્દિલા હવા અલા પ્રાથમ પ્રાથમ અલા પ્રાથમ અને લાગ પ્રાથમ અને પ્રાથમ પ્રાથમ હ
Arg426-Lys432	(881)	ending of the Algeria of the control
Arg426-Gly431B	(881)	(writer constructional attentions research (Governmette sylphone
Asn425-Lys432	(881)	макечайсь таклюўно подменты чаны начасі яканс
Consensus	(881)	CCCGCCCCAACAACACCCCGCAAGAGCATCACCATCGG
	<b>, ,</b>	921 960
Ile424-Ala433	(921)	ANTICLE COURSE CONTINUE VIEW CONTINUES AND C
Trp427-Gly431	(921)	୭.୧.୧୯୯୯.୧୯୯୯.୧୯୯୯.୧୯୯୯.୧୯୯୭.୧୯୯୯.୧୯୯୯.
Gln422-Tyr435B	(921)	୶ଽଢ଼ୠଢ଼ଢ଼ଢ଼୶ଢ଼ଢ଼୷ଽ୴୳ଽ୷୷ଽୡଢ଼ଽୡୢ୵ଢ଼୷ଢ଼ଢ଼ଽ୷୷୵ଽୡୢ୴ୢୡୡଢ଼ଢ଼
Arg426-Gly431	(921)	र्यतस्य सम्पर्धस्य स्थलान्य । भागतमान्य स्थलान्य स्थलान्य स्थलान्य स्थलान्य स्थलान्य ।
Ile423-Met434	(921)	A BOTA MATERIAL SERVICES OF SOME ASSESSMENT OF SERVICES OF SERVICE
Gln422-Tyr435	(921)	vacalejoina ejouraliseksijoide una verijudi, voeskijsekelo e
Arg426-Lys432	(921)	rejuje lejen revejo kristi okolokom krijeje je prosi u evisto prije je je je je krije kojek je je je je je je j
Arg426-Gly431B	(921)	୍ଦ ଅଧିକାର ଓ ଜିଲ୍ଲ ପ୍ରତ୍ୟ ଓ ବିଲ୍ଲା ଓ ଅଟେ ଅନ୍ତର୍ଶ କଥା । ଅଧିକ ଅଧିକ ଅଧିକ ଅଧିକ ଅଧିକ ଅଧିକ ଅଧିକ ଅଧିକ
Asn425-Lys432	(921)	referenced a complete in the contract of the c
Consensus	(921)	CCCCGGCCGCCTTCTACGCCACCGGCGACATCATCGGC
	•	961 1000
Ile424-Ala433	(961)	stantes delegation deservoires artistes autor quastrations
Trp427-Gly431	(961)	eMesters releje Meleje (837/0: neje. M/caix (337/0: rejeje je viet Antalia
Gln422-Tyr435B	(961)	statistic concernation were releasing the properties of the contraction of the contractio
Arg426-Gly431	(961)	Sylvatines reference consistent elegants and conversa forthe elegants and a
Ile423-Met434	(961)	Averages an enveloped electricate and enveloped and electricate and enveloped and electricate
Gln422-Tyr435	(961)	and the selection of the construction of the selection of
Arg426-Lys432	(961)	
Arg426-Gly431B	(961)	PROPAGE SACIENCE SERVICE PER MANAGEMENTA CONTRACTOR GRANGEN AND DE
Asn425-Lys432	(961)	elyayingan gentelede anangentengangangangangan
Consensus	(961)	GACATCCGCCAGGCCCACTGCAACATCAGCGGCGAGAAGT
		1001 1040
Ile424-Ala433	(1001)	downing your density and was the call contract, the contract of the call and the ca
Trp427-Gly431	(1001)	ૡ૱ <i>ઌઌઌ૱</i> ૢઌઌૡૡૡૡઌઌૡ૱ઌઌ <i>ૡ</i> ૱ૡૡૡૡૡૡૡૡૡૡ
Gln422-Tyr435B	(1001)	લંભમ્પ્રજામાં ભાગવાના માત્રમાં ભાગમાં ભાગમાં છે. તેમ જ તાલુકામાં તેમ જ તાલુકામાં ભાગમાં ભાગમાં ભાગમાં છે. જે ત
Arg426-Gly431	(1001)	eleanalestatarasiasicionreataricia-terpasiejinaaticiastaticiastrosaticiasticia
Ile423-Met434	(1001)	devaluatementales van bemarente en verte en ver
Gln422-Tyr435	(1001)	લે <b>કોમાં</b> ઈ:જેમાં સ્તાર કાર્યા કાર્યા છે. કાર્યા માના કાર્યા હોય છે. કાર્યા હોય કાર્યા હોય કાર્યા હોય કાર્યા હોય ક
Arg426-Lys432	(1001)	લેલોમાં/લામાં/લેપાલસંકાલસંકાયલોમાં લેલોમાં કર્યા છે. જે જે લેલો કર્યા છે. જે જે લેલો કર્યા છે. જે જે લેલો કર્ય
Arg426-Gly431B	(1001)	ddiariching cherandonich bir chranchrangstraß teles
Asn425-Lys432	(1001)	alethate to the little of the little of the value the enable in the little of the litt
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Consensus	(1001)	GGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGC
T1 404 D1=433	(1041)	1041 1080
Ile424-Ala433	(1041)	स्वराक्तकृतवादीवार्यमध्येत्रविवाद्याः भिववयम् वृत्यस्य स्वराम्यवयम् । इ.स.च्याक्तकृतवादीवार्यमध्येत्रविवादीवार्यस्य स्वराम्यवार्यस्य ।
Trp427-Gly431	(1041)	%ः।तस्याः श्रवतानः प्रयोककृ∫होत्रश्रेः स्टः स्टः स्टः स्टरः स्टरः स्टरंगान्तरा स्टर्गान्तरा स्टर्गान्तरा
Gln422-Tyr435B	(1041)	dertheimheigele marshayerangermannan mennangeritzanelenter
Arg426-Gly431	(1041)	Representative majories and continuous and activities of the contractive and c
Ile423-Met434	(1041)	Sentennia de la
Gln422-Tyr435	(1041) (1041)	Serial relations of the series
Arg426-Lys432 Arg426-Gly431B	(1041)	SATERIAL CONTRACTOR AND
Asn425-Lys432	(1041)	SCHOOL STANDON STANDARD STANDERS AND CONTRACTOR STANDARD
Consensus	(1041)	CCAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAG
Consensus	(TO41)	1081 1120
Ile424-Ala433	(1081)	RECERCION CONTRACTOR OF THE STANDARD CONTRACTOR
Trp427-Gly431	(1081)	destaction vector destatatement con ventral and contraction as
Gln422-Tyr435B	(1081)	न्यः संदर्भवरात्वाद्ववद्ववद्वर्भित्रवद्यात्मारः द्वद्यत्वर्भवर्भवर्भाः
Arg426-Gly431	(1081)	deletageavedsstallavevsasstamaavavastesenastanada
Ile423-Met434	(1081)	decides excelled y extraction of the contraction of
Gln422-Tyr435	(1081)	elegate entre collette (enrety enrighte en martielle en
Arg426-Lys432	(1081)	adeachance condition to the many many many many many
Arg426-Gly431B	(1081)	deserges integrandandes control action en en encomment
Asn425-Lys432	(1081)	વન્ય ભવન લાગ એક સંભૂતભાષાલ અલગ જેલા હતા ગામ સંખ્યામાં ઉપયોગી પોલિસ
Consensus	(1081)	GGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG
001.501.045	(100,1)	1121 1160
Ile424-Ala433	(1121)	લાહોદારાં અંતર ભાગમાં લાગ જ જ જ જ જ જ જ જ જ જ જ જ જ જ જ જ જ જ જ
Trp427-Gly431	(1121)	energy and the contract of the
Gln422-Tyr435B	(1121)	atticianad debish imbose versida eth salar atan aresistich skehilikere.
Arg426-Gly431	(1121)	નહિલ્લાના સામાના કરેલા છે. તેમ જ જો લાગ કરાયા છે. જો કરાયા
Ile423-Met434	(1121)	ejelelet overhelet stemme milyember avgrenne seglet och fer ombetann et i
Gln422-Tyr435	(1121)	dedictions of contrations to a various transfer of the
Arg426-Lys432	(1121)	School Characterical Carles Compact Anna Carles Car
Arg426-Gly431B	(1121)	disease to the unconsiderate increases with a second contestine on a
Asn425-Lys432	(1121)	Activities Production and Conference of the Conf
Consensus	(1121)	GCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAA
	•	1161 1200
Ile424-Ala433	(1161)	system (s,t) + system (s,t) + t + t + t + t + t + t + t + t + t +
Trp427-Gly431	(1161)	AND CONTRACTOR OF THE PROPERTY
Gln422-Tyr435B	(1161)	tificial prima equivalent et et prima protection production et et protection et et et protection et et et protection et
Arg426-Gly431	(1161)	structure and ethicitistic properties and construction of the state of
Ile423-Met434	(1161)	sales in a nation of the supersymptotic constraint with the
Gln422-Tyr435	(1161)	witelestere san feriviser wite successiville feet of each contract private in text.
Arg426-Lys432	(1161)	as the sign of a rectangue to the second control of the state of the second sec
Arg426-Gly431B	(1161)	MACCONSTRUCTION OF THE CONTRACT OF THE CONTRAC
Asn425-Lys432		avecuvers mecenyaternatable enhaltere conditions well to be
Consensus	(1161)	CAGCACCTGGAACAACACCATCGGCCCCAACAACACCAAC
		1201 1240
Ile424-Ala433	(1201)	वृद्धारात्रात्रात्रात्रात्रात्रात्राद्धात्रात्रस्यवादात्र्रात्रस्य विद्यात्रात्रात्रात्रात्रात्रात्रात्रात्रात
Trp427-Gly431	(1201)	Helpherm consequences action of the same was a second contract to the same of
Gln422-Tyr435B	(1201)	Scovering Market and Control of the State
Arg426-Gly431	(1201)	ૡૢૡ૽૱ૺઌૡઌ૱ૡૡઌૺૡૡૡઌૡૡ૽ૹૡૺ૱ૡૡ૱ૡૡ૱ <i>ૢ</i> ૱૱ૹઌૺૡઌઌ૽ૢૡઌૡઌ૱૱ૺ
Ile423-Met434	• •	Security of the control of the second of the
Gln422-Tyr435	(1201)	egovern and standard control of
Arg426-Lys432	(1201)	algeryetetetetituretakoloota kalotoloota taratitatei istelekiila iteksii.
Arg426-Gly431B	(1201)	actives intolicitals conficial environment and
Asn425-Lys432	(1201)	GCONCONTENCING STEERING CONTENTS TO A CONCONTENT OF THE A TOP
Consensus	(1201)	GGCACCATCACCCTGCCCTGCCGCATCAAGCAGATCATCA 1241 1280
		1280

FIG. 4F

Ile424-Ala433	(1240)	
Trp427-Gly431	(1241)	TGCGCTGG द्विष्ठे के ताल के अधिवास लाहर महिल्ला कर महारा द्वारा है।
Gln422-Tyr435B	(1234)	GC GCC B WAS TO SEE SE SE SUIT SE
Arg426-Gly431	(1241)	TOCGCGCC GGGGGG% AFIGGGGAAACAACAACAACAACAACAACAACAACAACAACAA
Ile423-Met434	(1237)	Gelelele Amanatematicalacticalactic
Gln422-Tyr435	(1234)	
Arg426-Lys432	(1241)	AGCGCGGC EGGAA ON TEGRES TREST SECTOR EN ELECTRONICATION
Arg426-Gly431B	(1241)	AGCGCGGCA GGGGAAGGGAAGCTAAGCGGAAGCAAAG
Asn425-Lys432	(1241)	1/6
	- •	
Consensus	(1241)	
	410601	
Ile424-Ala433	(1269)	्रविदाहरु,गर्भगम्बालविदासद्यक्षेत्रम्बदाग्रहरू,गर्भग्रह,ग्रवकरावेच्छ ग्रह्मान्।
Trp427-Gly431	(1281)	्रविद्यसम्प्रतारमञ्जूषारम् स्वयम्भवत् । स्वयम्
Gln422-Tyr435B	(1257)	nemental encommental enternation de la competité des la competité des la competité de la competité des la competité des la com
Arg426-Gly431	(1281)	सहार १९७५ विकास होता है। असे विकास को उसके असे का की स्वार की है।
Ile423-Met434	(1263)	eldid molytic in reference mental control of the research of t
Gln422-Tyr435	(1257)	लब्रह्म क्षेत्र क्षेत्र का स्टब्स का स्टब्स का स्टब्स का क्षेत्र का अपने का स्टब्स का स्टब्स का स्टब्स का स्टबस
Arg426-Lys432	(1281)	अविद्यांदर्भारत्वेतात्वंद्यादर्भवदर्भवदर्भवदर्भवदर्भात्वर्भवदर्भवदर्भवदर्भवदर्भवदर्भवदर्भवदर्भ
Arg426-Gly431B	(1281)	Germannerender bei der bei der ber ber ber ber ber ber ber ber ber b
Asn425-Lys432	(1275)	founditions contact wileth with the transfer contact of
Consensus	(1281)	CGGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTG
30	, ,	1321 1360
Ile424-Ala433	(1309)	esteres releative defectes and estimates in the interior of increase
Trp427-Gly431	(1321)	within a successful decided in Available and a secretion of the contraction of
Gln422-Tyr435B	(1297)	weakenededyseacedae.wytercereterassaequesser.
Arg426-Gly431	(1321)	ක්වස්/වූවම ස්ලක්/ස්ස්පුව්වය සමාවේ සමාව දැන්ව දැන්වේ දැන ස
Ile423-Met434	(1303)	entervision enteres enteres enteres mentionales est
		ENHALEGICACHUCAGACHACHACHACHACHACHACHACHACHACHACHACHACHA
Gln422-Tyr435	(1297)	Contract of the contract of th
Arg426-Lys432	(1321)	: અમુલાયા લાગુ છે. લાગુ કર્યા લાગ્યા લાગુ લાગુ છે. તે કર્યા લાગુ લાગુ લાગુ કર્યા છે. જે છે. જે છે. જે છે. જે છ
Arg426-Gly431B	(1321)	० ॥ कोरविवयद् ल <b>क्षेत्रसम्बद्धान् ।</b> स्थानम् दश्यानः अस्य अस्य अस्य स्थानस्य स्थानस्य ।
Asn425-Lys432	(1315)	enelystedanyasdenosystanassissyssystysas
Consensus	(1321)	CTGACCCGCGACGCGCAAGGAGATCAGCAACACCACCG
	-	1361 1400
Ile424-Ala433	(1349)	प्रकारक कार स्वतन्त्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्वतंत्र स्
Trp427-Gly431	(1361)	destinguished control of the respondence of the section of the section of
Gln422-Tyr435B	(1337)	Methods instruction detailers election handwick, electronistics
Arg426-Gly4 <b>31</b>	(1361)	House, conscionate interior de classicies de la forma que la fattalist de mé
Ile423-Met434	(1343)	Historical references control of the particular to
Gln422-Tyr435	(1337)	Mathematic general entrangement of the property of
Arg426-Lys432	(1361)	Value confolicio de la principa de la companio de la contrata del la contrata de la contrata del la contrata de la contrata del la contrata de la contrata del la contr
Arg426-Gly431B	(1361)	अस्तरकार आस्ति व्यवस्थित वार्य विद्यान वार्य क्षेत्रकार स्थापन स्थापन स्थापन स्थापन स्थापन स्थापन स्थापन स्थाप
Asn425-Lys432	(1355)	iteration in the energy are accidentially interested to the energy of th
Consensus	(1361)	AGATCTTCCGCCCCGGCGCGCGACATGCGCGACAACTG
	-	1401 1440
Ile424-Ala433	(1389)	Selection and a superior of the superior and an action of the superior and action of the superior action of the superio
Trp427-Gly431	(1401)	STOCK TASK CANTON CONTROLLED STATE OF THE CHARLEST CONTROLLED TO THE
Gln422-Tyr435B	(1377)	chielestics (citieles phytes etemps diesferen, eleakes freinke est re
Arg426-Gly431	(1401)	HEIGHEN MENTELEN BURNER FOR FOR FOR FOR MENTELED FOR
Ile423-Met434	(1383)	elefeleiteleiteleitelefahrteitelefahreiteteleftelefahreitetete
Gln422-Tyr435	(1377)	addryctayddianyriyyanionyradniachalygyddiacyr
Arg426-Lys432	(1401)	dedestidicistacifaktussistejkteisistelektustaikitaikijatok
Arg426-Lys432 Arg426-Gly431B	(1401)	descinational of the same of the same same same same same same same sam
		Secularies de la constant de la cons
Asn425-Lys432	(1395)	GCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAG
Consensus	(1401)	
Ile424-Ala433	(1429)	ૹૡૡૡૡૡૡૡૡૡૡૡઌૣૹ <i>૽૽૱૱</i> ૹ૽૽ૢ૽૱ઌઌૡ૽૽ૡઌૹઌૹૡ૽૽ૡૡૡૡૡૡ
Trp427-Gly431	(1441)	ल्लान्त्रभावत् वर्षात् । इति

FIG. 4G

Gln422-Tyr435B	(1417)	संबेधसम्बद्धायस्थितं होत् होत्। होत्या क्षात्राच्या होत्या होत्या होत्या होत्या होत्या होत्या होत्या होत्या होत
Arg426-Gly431	(1441)	decented and added to the authority decided and accompanied
Ile423-Met434	(1423)	ार्गर-अन्तर्भवस्थान्त्रभृतवान्तर्गराज्यात्रस्थात्रस्थात्रस्थात् ।
Gln422-Tyr435	(1417)	सर्दर अपन्यत्वर देवर देवर दिन्द्र । त्या क्षेत्र व
Arg426-Lys432	(1441)	चर्त्यहम्भेलवेल्हासम्बद्धांचलाहाल्टाकार्यःच्यार्थःच्याराहाम् <mark>यात्वेल्लाल्यात्वार</mark> ्यम्
Arg426-Gly431B	(1441)	white declarance application with three that yet applicate the
Asn425-Lys432	(1435)	REGINACE CONTROL CONTR
-		<del></del>
Consensus	(1441)	CCCCTGGGCGTGGCCCCACCAAGGCCAAGCGCCGCGTGG
		1481 1520
Ile424-Ala433	(1469)	য়ঀ৾ড়ঀঀঀড়য়ঀড়য়ঀৢড়য়ৣঀঀ৾ড়ড়৸ঢ়ড়ড়ড়৸ঢ়ড়ড়ড়ড়ড়ড়৸ৼঢ়৸৸
Trp427-Gly431	(1481)	त्वकर दब्दादिए प्रवस्तावर वर्षाद्या । वर्षाद्वाद्यवद्याद्यवद्याद्यवद्याद्य
Gln422-Tyr435B	(1457)	मुल्कार्यक्रिक्ट्रिक्ट्रिक्रिर्द्रद्रवालास्ट्राक्ट्रिक
Arg426-Gly431	(1481)	telestected and addiction in the contract of t
Ile423-Met434	(1463)	n,elowevelouschedemelendomenter/neteinjdelendelenterinket in
Gln422-Tyr435	(1457)	RECORD CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR
Arg426-Lys432	(1481)	। इत्राह्मा स्थान स्
Arg426-Gly431B	(1481)	(କ୍ଷୟମମସ୍ପର୍ଗୟର ଅନ୍ତିପ୍ରକ୍ତ ଅନ୍ତମନ୍ୟ ପ୍ରତମନ୍ଦ୍ରପ୍ରପ୍ରକ୍ତ ହେଉଛି ।
Asn425-Lys432	(1475)	तस्तित्रतत्रवस्य (केप्रमान प्रवाद्य विद्याचा अस्त्रप्रवाद वित्रप्रवाद व्यवस्था ।
Consensus	(1481)	TGCAGCGCGAGAAGCGCGCGTGACCCTGGGCGCCATGTT
Consensus	(1401)	1521 1560
T1 . 404 . B1 = 433	(1500)	
Ile424-Ala433	(1509)	ः व्यवस्थान् । प्रतिकृतिक स्थाने स्थाने स्थाने स्थाने स्थान
Trp427-Gly431	(1521)	તું કુંમારાનું દિલ્લા ૧૦૦૦ કરીય <b>લા (</b> ક્લા) (૧૦૦૧ વિજયના ૧૯૧૧ માટે છે. માટે કર્યા વાસ <b>કરો</b> છે. માટે કર્યા છે.
Gln422-Tyr435B	(1497)	assicular considerad returnonida istribetadas
Arg426-Gly431	(1521)	contraction of electric confidency and the electric contractions of the electric contraction of the electric contr
Ile423-Met434	(1503)	entanda a en la facilitation de la contrata del contrata de la contrata de la contrata del contrata de la contrata del la contrata de la contrata del la contrata de la con
Gln422-Tyr435	(1497)	Noveletic www.comededecticandedectics.com/sedectics.com
Arg426-Lys432	(1521)	<i>्रक्तरहात्त्वातः ५५००० द्वासा</i> ल्यस्य व्यवस्थात् ।
Arg426-Gly431B	(1521)	wealted a characteristic content of the state of the stat
Asn425-Lys432	(1515)	POTESCO POCTOS EPOPOS SEGONIZADO A TRES ESCO
Consensus	(1521)	CCTGGGCTTCCTGGGCGCCGCCGGCAGCACCATGGGCGCC
	,	1561 1600
Ile424-Ala433	(1549)	decidental city formatted by a structure of the material
Trp427-Gly431	(1561)	designations and an emphasical and an experience of the experience of
Gln422-Tyr435B	(1537)	ଽଽ୵୶୷୶୷୶୷ଡ଼୷ଡ଼୷୷୶୷ୣ <b>ଡ଼୵୰</b> ଽୡୢଽଽ୷୷ୠ୕ଽ୕୴୕ଽୠୠ୷୶୷ <del>ୡଽୡଽ</del> ୡ୷ଌୄ୷
Arg426-Gly431		Sastricionistrolenemente contracceriación deniament
-	(1561)	spent of the partie of the control o
Ile423-Met434	(1543)	
Gln422-Tyr435	(1537)	entities in the state of the st
Arg426-Lys432	(1561)	न्यं कर्मात्राक्षात्रम् । तं व्यक्षित्रम्य व्यक्षित्रम्य । व्यक्षित्रम्य ।
Arg426-Gly431B	(1561)	efficient efficient autority effect estates effects estates en fait en en fait
Asn425-Lys4 <b>32</b>	(1555)	contened at the feature of the contened of the second of the contened of the c
Consensu <b>s</b>	(1561)	CGCAGCCTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGA
		1601 1640
Ile424-Ala433	(1589)	यञ्चरपुरक्षकर्वाद्यसम्बद्धानसम्बद्धानम् । जनस्यसम्बद्धानसम्बद्धानसम्बद्धानसम्बद्धानसम्बद्धानसम्बद्धानसम्बद्धान
Trp427-Gly431	(1601)	essection and majorites that the transfer and characteristic to
Gln422-Tyr435B	(1577)	HER GOOD WINDOWS CHONGO WOND WIND WERE GREET HER CONTROL OF THE CO
Arg426-Gly431	(1601)	ewalerst alle die multischter einhautwirken bereichte der
Ile423-Met434	(1583)	dicterior and and resident properties and assessment and a significant
Gln422-Tyr435	(1577)	दृहर्द्धातिकः स्थान् व्याप्तकः स्थान्य । स्थान्य विद्यान्तिकः स्थान्य । स्थान्य । स्थान्य । स्थान्य । स्थान्य
Arg426-Lys432	(1601)	SEMPLEASING CHOOMERAGE AND AND ASSOCIATED SHOP CHOOLES AND
Arg426-Gly431B	(1601)	
Asn425-Lys432	(1595)	ECOCOS CONTRACTOR ACTIVACION CONTRACTOR CONT
Consensus	•	GCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCCCAT
consensus	(1601)	
T1 - 404 - 51 - 400	/1 (20)	
Ile424-Ala433	(1629)	<u> </u>
Trp427-Gly431	(1641)	owners were control of the control o
Gln422-Tyr435B	(1617)	न्त्रभृत्यत्रः अर्थववभूयवन्त्रभयः १४०८-१४वन् १४वन् १४वन् ।
Arg426-Gly431	(1641)	ल्खारवादीयक इंडिंग्स्टक एक दर्शन , ये कर व, कराव, त्राचन , व्याचन , विभावसंस्थितिक ।
		510 411

FIG. 4H

Ile423-Met434	(1623)	SOVERESTIVATIVE OF CARLEST OF STREET OF STREET
Gln422-Tyr435	(1617)	अक्षेत्रवदातलक्षेत्रवक्षेत्रवक्षेत्रवक्षेत्रवक्षेत्रवदामबदाम्बद्धानाकाः विद्यविद्यक्षेत्रविद्यविद्यव
Arg426-Lys432	(1641)	
Arg426-Gly431B	(1641)	्रव्यवसम्बद्धाः स्वतः । स्वतः
Asn425-Lys432	(1635)	
Consensus	(1641)	
		1681 1720
Ile424-Ala433	(1669)	
Trp427-Gly431	(1681)	where where such the resulting error of the profession of the second ending
Gln422-Tyr435B	(1657)	
Arg426-Gly431	(1681)	୵୲୲୲ଽ୲୶୵୳ଽ୵୵୳ଽ୷୷୲ୡୢ୲୵ଢ଼ଢ଼ୡ୕ୡୗୠଵୡ୷୷୷ଢ଼ୠୡୣଌୡୡ <b>୕ୡ୷୵୶୕୷୷</b>
Ile423-Met434	(1663)	www.nec.yac.rde.Wedensicakolide.jce.comie <mark>dwe</mark> cid
Gln422-Tyr435	(1657)	෭෧෦෬෦෭෭෦෫෮෩෫෩෭෪෧෦෦෩෪෭෫෦෩෮෫෩෩෮෧෫෧෩෦෪෧෦෩෦ඁ <mark>෫෦ඁ෯෦෪෧</mark> ෦෨෧෦
Arg426-Lys432	(1681)	tARCOTATE USTACLO ACCIDAC QUE CANCIAN NEUN CELIN CELINGENTO COLONIA
Arg426-Gly431B	(1681)	An anticolyme tandanetagede sechadenendalance in
Asn425-Lys432	(1675)	ઋત્લાસ્ત્રીવીસમાવદાતલહા/દામુહેષ્ટ્રાહાલીદાવા વહાલાલા <mark>લા લેવમાં વેલાવી</mark>
Consensus	(1681)	ATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCGCT
	,	1721 1760
Ile424-Ala433	(1709)	१/६/६८३५वारः वयः १८/६८१४वाः १८००। वर्षाः वत्तवातः १५००५ व्यवस्थान् ।
Trp427-Gly431	(1721)	ASSENTED A CONTRACTOR OF THE PROPERTY OF THE P
Gln422-Tyr435B	(1697)	uncinganu leucicaldour managedado propadiciones
Arg426-Gly431	(1721)	ACT THE CONTROL STATE AND ACT OF THE CONTROL OF THE
Ile423-Met434	(1703)	पुत्रक मान्य प्रमान वर्ष प्रतास प्रतास कर वर्ष वर्ष वर्ष वर्ष वर्ष अमान वर्ष वर्ष अमान वर्ष वर्ष मान्य प्रतास वर्ष प्रतास वर प्रतास वर्ष प्रतास वर प
Gln422-Tyr435	(1697)	ANOTO TRANSPORTED SERVICE OF THE SER
Arg426-Lys432	(1721)	The without of the factor of t
Arg426-Gly431B	(1721)	
Asn425-Lys432	(1715)	Agricultudo en el decidente de desente de la constante de la c
Consensus	(1721)	ACCTGAAGGACCAGCAGCTGCTGGGGCATCTGGGGCTGCAG
	• • • • • • • • • • • • • • • • • • • •	1761 1800
Ile424-Ala433	(1749)	Helesty, versus missions de catalon de la compania con de la confession de
Trp427-Gly431	(1761)	elelety to the east of elelelelety of the control established
Gln422-Tyr435B	(1737)	detectionally ground spicitional order of examining a designation
Arg426-Gly431	(1761)	ticle of any analytic postelety cyleratic principle sycherolayetes.
Ile423-Met434	(1743)	SCICOLARY (ARCHA CERNAL COLOR PROCESSOR SCIENTIFICAL
Gln422-Tyr435	(1737)	and the state of the solution of the state of the solution of
Arg426-Lys432	(1761)	and an experimental control of the c
Arg426-Gly431B	(1761)	Reference in employment of the control of the contr
Asn425-Lys432	(1755)	continuent de la contra la
Consensus	(1761)	CGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCC
		1801 1840
Ile424-Ala433	(1789)	The contribution of the contribution and contribute and contributions of the contribution of the contribut
Trp427-Gly431	(1801)	ાંલીલ જેલાન્ય કેલ જો કેફાલ જોડા કેલા કેલાલા કેલાલા કેલા છે. જેલા છે. જેલા કોલાફોર્ક સ્થાનિક કરો છે.
Gln422-Tyr435B	(1777)	ACIONE SACCOMISMACO ACICIO CENTO SALEMA CON PICTORIO DE LA COMPONIO DEL COMPONIO DE LA COMPONIO DE LA COMPONIO DEL COMPONIO DE LA COMPONIO DEL COMPONIO DE LA COMPONIO DEL COMPONIO DE LA COMPONIO DE LA COMPONIO DELIGIO DEL COMPONIO DELIGIO DELIG
Arg426-Gly431	(1801)	Trike negassaciesta izo yaktesta cicion neiessa elektreza esta elektrika estatuen
Ile423-Met434	(1783)	Heir ters regards by the best contact to the particular test for
Gln422-Tyr435	(1777)	Note the state of the participation of the state of the s
Arg426-Lys432	(1801)	Melecche confederation Mengelen einer sein vor anne melegraffen aus in
Arg426-Gly431B	(1801)	ne contelesticie insuestrinestrelesconeich sein siterrine in destrinestr
Asn425-Lys432	(1795)	ŊĊĠŖŖĠĸijĠſĸŊijĠĸĸijĠĸĬſĠſĠĸĠĠĊĸĸĠĸſĠĸŶŔĸĸŔĠſĠĨĸĬſĸĬŶĸĬĊŶ
Consensus	(1801)	AGCTGGAGCAACAAGAGCCTGGACCAGATCTGGAACAACA
		1841 1880
Ile424-Ala433	(1829)	त्रकारे राह्तभ्रद्धाने स्थापित क्षेत्रका विद्यास्त्र स्थापित क्षेत्र स्थापित क्षेत्र स्थापित स्थापित स्थापित स
Trp427-Gly431	(1841)	httyclementwiselettemonologyclolology charcestemonalisticste
Gln422-Tyr435B	(1817)	KGAYCO: » GONER GIGHTOR EGGENTAGO GIGGEN OFFIC GAMMAN GENTAGOTO
Arg426-Gly431	(1841)	AQMONTA ELEVARACAMENTA (CAMPENTA CAMPANTA CAMPANTA (CAMPANTA )
Ile423-Met434	(1823)	igativale interestabilitatival element in interestabilitatival element interestabilitativa element
Gln422-Tyr435	(1817)	headreposkelekture or den saletarien et ein orden den den deskelekteleke
•		

FIG. 4I

Arg426-Lys432	(1841)	.स.च.१०१०अस्यव्यः ११५४द्वेद्वः ११५६द्वेद्वः ११५६द्वः ११५५द्वः ११५५द्वः ११५८५
Arg426-Gly431B	(1841)	
Asn425-Lys432	(1835)	FOR ACTION OF THE PARTY OF THE PROPERTY OF THE PROPERTY OF THE PARTY O
Consensus	(1841)	TGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACAC
		1881 1920
Ile424-Ala433	(1869)	હ્યું, કાલો કાલો કાલો કાલો કાલો કાલો કાલો કાલો
Trp427-Gly431	(1881)	structing and high construction and a value of the fire
Gln422-Tyr435B	(1857)	लक्ष्मा १८६। में क्षा मा १८१६ में १८५ में १८६
Arg426-Gly431	(1881)	कोर्ग्या कर्मा प्रकार का को प्रकार को प्रकार के स्वापन को स्वर्ध के स्वर्ध के स्वर्ध के स्वर्ध के स्वर्ध के स्
Ile423-Met434	(1863)	ર, કર્માં ભારત કૃત્યા જ કરા કર્યા છે. તે કર્યા કૃતિ કૃતિ કૃતિ કૃતિ કૃતિ કૃતિ કૃતિ કૃતિ
Gln422-Tyr435	(1857)	waster reading president and state of the contraction of the contracti
Arg426-Lys432	(1881)	इस्यान्त्रियम् सम्प्रात्रे वर्षात्रे प्रकृतिक वर्षात्र प्रकृति । इस्यान्त्र स्ति । इस्यान्त्र स्ति । इस्यान्त्र
Arg426-Gly431B	(1881)	अभ्येतका स्वरायका स्वरायक स्वर
Asn425-Lys432	(1875)	<b>ૹ</b> ૹ૽ૹૡૡ૽ૡૡ૱ૡૡૹૹૹૹૹૡૡૡ૽૱૱ૡઌઌઌૹૡૹૡ૱૱ૹૹૹૹૹૹ
Consensus	(1881)	CAACCTGATCTACACCCTGATCGAGGAGGCCAGAACCAG
		1921 1960
Ile424-Ala433	(1909)	ancianamidividamentidamente radicamente diplompi
Trp427-Gly431	(1921)	NAGAYANYAGAYAGAYAGAYAGAYAGAYAGAYAGAYAGA
Gln422-Tyr435B	(1897)	संभूत्रविक्रात्रभू तक्षेत्रभूववेश्वर्यव्यक्ष्यत्वक्ष्यत्वे । यहन्यविक्रात्वक्ष्यत्वम्
Arg426-Gly431	(1921)	cyticles/espites/yejtylicie/destructures-notation-neletylytyles/
Ile423-Met434	(1903)	sityclustychtifusptychelest/contribity a e njejo salejtych nejedychtypyn
Gln422-Tyr435	(1897)	when you was a same of the same and the same of the sa
Arg426-Lys432	(1921)	कर्पाटक्षप्रसाकर्गसः अपूर्वातिकारकार्यासीक्षप्रदादः । । १८३६ - (६३१०) १५४४ द्वारात्रे स्थानिक
Arg426-Gly431B	(1921)	adja (chijesi). jedinijajaja i jakojajajaje njedenan ini com njedanje inijeni
Asn425-Lys432	(1915)	cruerrenrant mariders de troinne mainde pela de tratan
Consensus	(1921)	CAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGT
		1961 2000
Ile424-Ala433	(1949)	decisies/escances elemento conducto contrate estate interestrate decision
Trp427-Gly431	(1961)	eleta y estre y consequente establishes se se consequence o
Gln422-Tyr435B	(1937)	ପ୍ରଶିକ୍ତ ଓ ପ୍ରସ୍ତିକ । ପ୍ରସେଶ ଓ ପ୍ରସେଶ । ପ୍ରସେଶ ଓ ଅବସ୍ଥା ।
Arg426-Gly431	(1961)	द्रावाद्यविष्यात्रात्वाद्यं विषयः विषयः स्थाने
Ile423-Met434	(1943)	elegicionate, e constituto aprili proprio proprio proprio avalente.
Gln422-Tyr435	(1937)	station, writers, nearly considerable contraction of the single property with the second
Arg426-Lys432	(1961)	ed de cuite que constant de la const
Arg426-Gly431B	(1961)	delignerate en en contrante en
Asn425-Lys432	(1955)	Sadden Sage Lead Control of Contr
Consensus	(1961)	GGGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCT
T1-424 N1-422	(1000)	2001 2040
Ile424-Ala433	(1989)	thing controlly an extension resembles a function of a controlling of the
Trp427-Gly431	(2001)	देवराहर मध्य व्यवस्था व्यवस्था अभिनादा वर्षाता हेला वा इतमा मध्या इसिहार वर्ष
Gln422-Tyr435B	(1977)	engelengiyi issa, a <b>ya</b> tasa ayana (esahnan) istaya ayan di dista ci <b>eleleje</b> se
Arg426-Gly431 Ile423-Met434	(2001)	almetrative of technical sections is retrained to relatively or states (selections)
Gln422-Tyr435	(1983)	en en Austria, propieta esta esta en en en en en entre esta esta esta esta en en en entre esta esta esta esta e
Arg426-Lys432	(1977)	chne, chi www. www.cowingness.cowings.com. com completele ender
Arg426-Gly431B	(2001)	en de la
Asn425-Lys432	(2001)	A TOTAL PROPERTY OF THE PROPER
Consensus	(1995)	CARCOLLO MENTO POR MEMBER MENTO MENTO CARCOLLO COMO CARCOLLO CARCO
consensus	(2001)	GTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTG 2041 2080
Ile424-Ala433	(2020)	
Trp427-Gly431	(2029) (2041)	Shacker (activities) bith suffering haden selend. Asteine eine einstate in in the entry and an eine selend.
Gln422-Tyr435B	(2017)	
Arg426-Gly431	(2017)	CHARLES CONCRETE AND CONTRACTOR OF THE AND C
Ile423-Met434	(2023)	CARCACTOR AND CARCACTOR CARCACTOR CONTRACTOR
Gln422-Tyr435		energegen her de konstantenen konstantenen et en betreten beste de konstantenen beste best
Arg426-Lys432	(2017) (2041)	divergence de la compara de la
Arg426-Gly431B	(2041)	chacterial in the control of the con
Vrd450-GTA431B	(2041)	chilaleicicing almeiners ners anachaine i blace jedinariamen traichte nachanachangein

FIG. 4J

Asn425-Lys432	(2035)	द्यांत्रस्थान्तराष्ट्रस्ट स्टार्के स्टार्क स्
Consensus	(2041)	
		2081 2120
Ile424-Ala433	(2069)	
Trp427-Gly431	(2081)	
Gln422-Tyr435B	(2057)	The second secon
Arg426-Gly431	(2081)	
Ile423-Met434	(2063)	
Gln422-Tyr435	(2057)	AND ADDRESS OF THE PARTY OF THE
Arg426-Lys432 Arg426-Gly431B	(2081) (2081)	
Asn425-Lys432	(2075)	Todachiededo felas natureleadamente finadaven
Consensus	(2073)	ACCECTGCCCAGGCTACAGCCCCCTGAGCTTCCAGAC
0050545	(2001)	2121 2160
Ile424-Ala433	(2109)	ଶ୍ୟପ୍ତମାନ୍ୟମୟନ୍ତି ବ୍ୟୁଷ୍ଟରେ ପ୍ରଦ୍ୟୁ ପ୍ରମୟକ୍ଷ୍ୟ ପ୍ରସ୍ଥ ପ୍ରସ୍ଥ ପ୍ରଦ୍ୟୁ ଅନ୍ୟ ପ୍ର
Trp427-Gly431	(2121)	ପ୍ରତ୍ର ମଧ୍ୟର ଅନ୍ତର୍ଶ୍ୱର ପ୍ରତ୍ୟର ପ୍ରତ୍ର କରିଥିଲି ।
Gln422-Tyr435B	(2097)	෧෫෦෭෧෦෦෦෫෪෦෩ඁ෧෬෦෦෮෩෩෫෧෫෦෩෩෦෩෮෭෦෩෧෩෦෮෦෮෦෩ඁ෫ඁ෮෦ඁ෭ඁ෫ඁඁඁ෧ඁ෬෫
Arg426-Gly431	(2121)	<u>୶୲୶ୡଽୣ୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷୷</u>
Ile423-Met434	(2103)	ૹૢૹ૽૽ૡઌૡ૽ૺ૾ૹૹૡૡ૽ૡૡૹૹ૽ૡૺઌૡૡૡઌૹૹ <i>ઌૡઌૡ</i> ૡ૽ૡૢઌૹૢૡૡ <b>ૡૡ</b> ૣ૽૽ૺ૿
Gln422-Tyr435	(2097)	stacts and continued and compact of the continued of the
Arg426-Lys432	(2121)	वेशनुरुपात्रकार्यकार्वा अस्तर्वा हास्त्रकार्यकार्यकार्यकार्यकार्यकार्यकार्यकार
Arg426-Gly431B	(2121)	अभव्यक्ष्मां व्यवस्थात् । विद्यान् व्यवस्थात् । विद्यान् विद्यान् । विद्यान् ।
Asn425-Lys4 <b>32</b>	(2115)	ૹૹૡૹ૱૱ૡૡૡ૽ૡૢૺઌ૱ૢઌૡઌ૽ઌ૽ૡ૽ૡૡૡૡઌૡઌૹૡૡૡૹ <mark>ૹૡૡૡ</mark> ૡૡ
Consensus	(2121)	CCGCTTCCCCGCCCCCGCGCCCCGAGGGC
-1 .01 .00		2161 2200
Ile424-Ala433	(2149)	incereuramentelescorrecentivacións
Trp427-Gly431	(2161)	गाहित्य/हर्न्नभवन्भवद्यदेशहर्द्यक्षमभवदद्यक्षमभवद्यक्षम्
Gln422-Tyr435B Arg426-Gly431	(2137) (2161)	wittenenteminderendentemintentretaerendentemi
Ile423-Met434	(2143)	Viene Checes de Carcella Carden Carden
Gln422-Tyr435	(2137)	Western and the state of the st
Arg426-Lys432	(2161)	Assessmented complete and accordance of the second of the
Arg426-Gly431B	(2161)	service and entering some sold and an entering sold an entering sold and an entering sold an entering sold and an entering sold an entering sold and an entering sold and an entering sold an entering sold and an entering
Asn425-Lys432	(2155)	कृत्वसम्बद्धाः । स्वतः स्वतः स्वतः । स
Consensus	(2161)	ATCGAGGAGGAGGGCGCGACCGCGACCGCAGCA
		2201 2240
Ile424-Ala433	(2189)	doughwenteleasteleanteleantent en elle mentellaken die elle intelle
Trp427-Gly431	(2201)	gadedengampangamengles andoministels adamping
Gln422-Tyr435B	(2177)	वेद्याद्रियं द्राया विद्या
Arg426-Gly431	(2201)	elegence entergrande entergrande en entergrande en entergrande en entergrande en entergrande en entergrande en
Ile423-Met434	(2183)	युवादीबार क्षेत्रत व्यक्तिक स्टाव्य व्यव्यव्यक्ति व्यवस्था ।
Gln422-Tyr435	(2177)	determination of the state of the second of
Arg426-Lys432	(2201)	de de la compara de la comp
Arg426-Gly431B Asn425-Lys432	(2201)	de order i i ste interiori de la companio de la co
Consensus	(2195)	CONTROL CONTRO
consensus	(2201)	GCCCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACGA 2241 2280
Ile424-Ala433	(2229)	2280 CONCRETE ACCUSATE CONTRACTOR
Trp427-Gly431	(2241)	was actional control to the control of the control
Gln422-Tyr435B	(2217)	gentusquestes catachias tanta anticonstate de la folce de la catachia de la catac
Arg426-Gly431	(2241)	તું અનુ લુકાલ જ્યારા માટે કરવા છે. તેમ જ માટે કરવા માટે કરવા કરવા છે. તેમ જ માટે કરવા માટે કરવા કરવા માટે કરવા
Ile423-Met434	(2223)	govidalus van a se se lo heim and a vandro de comuner.
Gln422-Tyr435	(2217)	त्र्यातृहरूद्विक्तृद्विक्शाद्विद्विद्वित्वाहरूतः त्याच्यतः स्त्रत्वित्यत्रव्वित्वद्विद्विद्विद्व
Arg426-Lys432	(2241)	ल्कारदास्त्वात्वात्र्वात्रम् सन्तर्भन्तः । स्तर्भन्तः । स्तर्भन्तः । स्तर्भन्तः ।
Arg426-Gly431B	(2241)	ब्हे अद्यक्षित्रभ्यत्। क्षेत्रभ्यत्। अत्यक्ष्या स्थाप्ति । स्थाप्ति । स्थाप्ति । स्थाप्ति । स्थाप्ति । स्थाप्त
Asn425-Lys432	(2235)	eletificial decretation and in crete information is the contract checkenteleter
Consensus	(2241)	CCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCCTGCGC

FIG. 4K

		2281 2320
Ile424-Ala433	(2269)	चरत्रिंभी द्वार्र तहोक बचर भरेही दिलेही हर दहाई है। उप प्रतिकार विकास दिले महिला है।
Trp427-Gly431	(2281)	विश्वहर्तास्य महाक्षेत्रस्य स्वरूपका विद्यादात । स्वरूपका स्वरूपका स्वरूपका स्वरूपका स्वरूपका स्वरूपका स्वरूपक
Gln422-Tyr435B	(2257)	aucona incontantagenciconalizacione autoriale de carec
Arg426-Gly431	(2281)	attientalmennemnedingasteletennemnedatelende rae
Ile423-Met434	(2263)	Alected as calety reduction (see three sounderreduction
Gln422-Tyr435	(2257)	Quechaduncana hancameda carastricana que cinacina de la compania del compania del compania de la compania del la compania de la compania del la compania de
Arg426-Lys432	(2281)	अभिराज्य स्थित कर्म महामान साम्या विद्या करते । अस्य अस्य स्थान स्थान स्थान स्थान स्थान स्थान स्थान स्थान स्थान
Arg426-Gly431B	(2281)	assertion repeated the celebration of the contraction of the contracti
Asn425-Lys432	(2275)	त्यम्बरुतस्य क्षेत्रम् विकासम्बद्धाः स्थाने । त्याच्याः स्थाने । त्याः स्थाने । त्याः स्थाने । त्याः स्थाने ।
Consensus	(2281)	GACCTGATCGCCGCCCGCATCGTGGAGCTGCTGG
		2321 2360
Ile424-Ala433	(2309)	इंदास्त्यद्द्वत्य्वद्वात्रव्यवद्ववयव्यवद्वाद्यक्ष्यस्य स्थाद्याद्वा <mark>यवद्वात्रस्य</mark> स्य
Trp427-Gly431	(2321)	બદાનુ ઘળસાના ભાગ તામ માત્ર કરવા છે. જ તે પ્રતાસ વારા માત્ર કરવા છે. જે જે તે માત્ર કરવા છે. જે જે જે જે જે જે જ
Gln422-Tyr435B	(2297)	बस्दिद्धान्त्रवात्रकात्रवात्रकात्रकात्रकात्रकात्रकात्रकात्रकात्रक
Arg426-Gly431	(2321)	तक्ष्मानुराज्यात्रसम्बद्धाः स्वतिक्षां स्वतः । स्वतः १००० । स्वतं क्षात्रः । स्वतं विद्यानुराज्यः ।
Ile423-Met434	(2303)	adelen elektionen elektrick elektrik (en tentalisisistiken).
Gln422-Tyr435	(2297)	स्लास्यकृत्याच्यास्याम् स्वतंत्राम् विवासम्बद्धाः । स्वतंत्राम् । स्वतंत्राम् । स्वतंत्राम् । स्वतंत्राम् । स्
Arg426-Lys432	(2321)	enceture, ence and electron contrated in west elected by (electron
Arg426-Gly431B	(2321)	त्रविक्तवित्रवित्रवेदकः असेत् । स्वेतव्यवकाः सः स्वरूप्तान् । स्वरूप्तान् स्वरूप्तान् स्वरूप्तान् स्वरूप्तान् स
Asn425-Lys432	(2315)	त्रहान्त्रहार्यात्रहेन्द्रम् क्ष्यं स्वयं स्वर्गेष्यं विद्यात्रहार स्वरं १००० हर्षा स्वरं स्वरं स्वरं स्वरं १००
Consensus	(2321)	GCCGCCGCGCTGGGGGCAACCT
		2361 2400
Ile424-Ala433	(2349)	entrantementer axente a transcriteration (en ala alteriale especies)
Trp427-Gly431	(2361)	स्टम्बर प्रकार क्षा का संस्था स्टब्स्ट अस्टा स्टब्स्ट अस्ट के स्टब्स्ट प्रकार प्रकार स्टब्स्ट स्टब्स्ट स्टब्स्
Gln422-Tyr435B	(2337.)	Resident outside sequences of the second content of the second con
Arg426-Gly431	(2361)	en kalendann mastrikolendilan kalenda attenta attanza eaglata ka
Ile423-Met434	(2343)	egytte oggennturkete synkerike er hen valerik og det et et et er
Gln422-Tyr435	(2337)	etralletesy experimental proposition and the contract of the c
Arg426-Lys432	(2361)	was certic attached in a contrate of the contr
Arg426-Gly431B	(2361)	चक्रत्रवार करवेते स्टब्स्टर स्टब्स्टर को क्रिक्टर स्टब्स्टर के स्टब्स्टर के स्टब्स्टर के स्टब्स्टर के स्टब्स्टर
Asn425-Lys432	(2355)	ete keleteraki keleteka kelean dan dan berkeleh keletek belan dan delektik belan dan delektik belan dan delekt
Consensus	(2361)	GCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTG
		2401 2440
Ile424-Ala433	(2389)	recovering et/class procedures and general designation is
Trp427-Gly431	(2401)	ACCIONES SE CONCIONES A CICIONAS ENCICIONAS CONCIONAS CONTRACADOS CONTRACIONAS CONT
Gln422-Tyr435B	(2377)	वेस्त्रकारकारकार <b>कार</b> सवाद्यक्षिणच्यास्य स्थान स
Arg426-Gly431	(2401)	Reference the Houte Legal Control State Control Contro
Ile423-Met434	(2383)	real enterior interior interior cut, and enclose interiors
Gln422-Tyr435	(2377)	में लेला है के का कार कि के कि कि के कि
Arg426-Lys432	(2401)	WHEN THE CONTRACTOR OF STREET STREET STREET, CONTRACTOR OF
Arg426-Gly431B	(2401)	representation to the classic contraction of the co
Asn425-Lys432	(2395)	adection in the vertical professional designation of the profession of the professio
Consensus	(2401)	AGCCTGTTCGACGCCATCGCCATCGCCGTGGCCGAGGGCA
		2441 2480
Ile424-Ala433	(2429)	व्यवसार्वास्य क्षेत्रका क्षेत्र विद्यार स्वतः स्व
Trp427-Gly431	(2441)	geler melce yegestyrclestelensche amvehelen gestellen achter
Gln422-Tyr435B	(2417)	ที่ตรมการรับกรุงกระการราชสหาริสตราย, การสุดสุดภูทินตสิสตร์สิตธ.
Arg426-Gly431	(2441)	૽ૣઌ૱૱ૡૡ૱૽૱ૹ૽૽ઌ૽ૢૡૡૺઌૡૺ૱ૡૡૡૺ૱ઌૡૺૡૡ૱ઌૡૺૡૡ૽ <b>ૡૡૺૡ</b> ૡૡ
Ile423-Met434	(2423)	sachmetalens divite (divine, encountries de mandalen el de contra la contra de la contra la contra de la contra del la contra de la contra de la contra del la contra de la contra de la contra de la contra del la contra de la contra del la contra de la contra del la contra de la contra del la contra de la contra de la contra de la contra del la cont
Gln422-Tyr435	(2417)	
Arg426-Lys432	(2441)	ञ्जलका/भेरावाकः स्तितंत्रका कर्याका स्वास्त्रका अने स्वास्त्रका स्थानिक स्वास्त्रका स्थानिक स्वास्त्रका स्थानिक
Arg426-Gly431B	(2441)	इस्त्वयहरूपसम्बद्धाः स्थापनः स्टाइट्टाइस्टाइस्टाइस्टाइस्टाइस्टाइ
Asn425-Lys432	(2435)	दर्भभगोतः वर्षप्रकारम् संबर्भसस्य स्वित्वा तर्पत्रस्य स्वतः स्वतः स्वतः स्वतः स्वतः स्वतः स्वतः स्वतः स्वतः स
Consensus	(2441)	CCGACCGCATCATCGAGGTGGCCCAGCGCATCGGCCGCGC
		2481 2520
Ile424-Ala433	(2469)	न्त्रामान्त्रकारात्रात्रात्रात्रात्रात्रात्रात्रात्रात

FIG. 4L

Trp427-Gly431	(2481)	<b>ंशक्तरः इत्सर्दिक</b>	Herrincicketeringstere	विक्रमण्ड <b>्ल</b> े	नद्दादशप्रमेखदाग्रद
Gln422-Tyr435B	(2457)	CHAIRSON KEICH	Kestaries es es este es es	activitie consideration	भुद्धाः <sub>भ</sub> भूद्धाः । १८
Arg426-Gly431	(2481)	STREET, SCHOOL	Activities classicistics	म्हरूर १० महाराजा स्थ	Acheria Reference
Ile423-Met434	(2463)		ter-project cicles of		
Gln422-Tyr435	(2457)	SHEED HELD	Anthropological	econscionation	त् <b>त</b> कारमञ्जलकार
Arg426-Lys432	(2481)	THE CHECK	ACMARIGIE CLESCHE	ल,एक (एक ले) स	describe carre
Arg426-Gly431B	(2481)	स्थापहरूपहरू	A Melelolologe of	AWERREDIC	SCENE CONC
Asn425-Lys432	(2475)	e interice	NEAVINGER (CCC)	WAS CONCEDENCE	SEE PROCESS
Consensus	(2481)	CTTCCTGC	ACATCCCCCGCCC	CATCCGCCAG	GCTTCGAG -
		25 <b>21</b>	2541	Ţ	
Ile424-Ala433	(2509)	ejejejejejeje pil	elo-Act a Delo-Kelta Ve	ł	
Trp427-Gly431	(2521)	संस्थलको स्थल हुए। इस्ट्राली स्थल हुए।	स्टाम्सम्बद्धाः <b>१</b> ८०० वस्य		
Gln422-Tyr435B	(2497)	अविद्यात किंग्रिकी	ANTIGARY TO THE STATE OF		
Arg426-Gly431	(2521)	defele ele en	HOWEVER TOWN FER W		
Ile423-Met434	(2503)	GERRICHER	asangah katak antah	ì	
Gln422-Tyr435	(2497)	week contract	e versions reserve	ľ	
Arg426-Lys432	(2521)	द्रदिश्चित्र क्षेट्र स्थ	elencetin 4//ches x //c	ł	
Arg426-Gly431B	(2521)	SCHOOL KON	SER HERRAYAVE DESIGNA		
Asn425-Lys432	(2515)	र्यद्विल्द्रस्थल्याम्	de-readiavement.		
Consensus	(2521)	CGCGCCCTC	CTGTAACTCGAC	3	

FIG. 4M

WO 00/393 <b>03</b>	-0		PCT/US99.
	28	/ <sub>1</sub> 65	. 30
Leu122-Ser199-Tryp427-Gly431	(1)	GAATTC	GCCACCATGGATGCAATGAAGAGA
Val127-Asn195-Arg426-Gly431	(1)	GAATTC	GCCACCATGGATGCAATGAAGAGA
Val120-Thr202-Ile424-Ala433	(1)	GAATTC	GCCACCATGGATGCAATGAAGAGA
Leu122-Ser199-Arg426-Lys432	(1)	GAATTC	GCCACCATGGATGCAATGAGAGA
Leu122-Ser199-Arg426-Gly <b>43</b> 1	(1)	GAATTO	GCCACCATGGATGCAATGAAGAGA
Lys121-Val200-Asn425-Lys432	(1)	GAATTC	GCCACCATGGATGCAATGAAGAGA
Val120-Ile201-Ile424-Ala433	(1)	GAATTC	GCCACCATGGATGCAATGAAGAGA
Val120-Ile201B-Ile424-Ala433	(1)	GAATTC	GCCACCATGGATGCAATGAAGAGA
Consensus	(1)	GAATTC	GCCACCATGGATGCAATGAAGAGA
		31	60
Leu122-Ser199-Tryp427-Gly431	(31)	GGGCTC	TECTETETECTECTETETEGA
Val127-Asn195-Arg426-Gly431	(31)	GGGCTC	TGCTGTGTGCTGCTGTGTGGA
Val120-Thr202-Ile424-Ala433	(31)		TGCTGTGTGCTGCTGTGTGGA
Leu122-Ser199-Arg426-Lys432	(31)	GGGCTC	TGCTGTGTGCTGCTGTGTGGA
Leu122-Ser199-Arg426-Gly431	(31)	GGGCTC	TGCTGTGTGCTGCTGTGTGGA
Lys121-Val200-Asn425-Lys432	(31)		TGCTGTGTGCTGCTGTGTGGA
Val120-Ile201-Ile424-Ala433	(31)		TGCTGTGTGCTGCTGTGTGGA
Val120-Ile201B-Ile424-Ala433	(31)		TGCTGTGTGCTGCTGTGTGGA
Consensus	. (31)	. / 4	<b>IGCTGTGTGCTGCTGTGTGGA</b>
		61	90
Leu122-Ser199-Tryp427-Gly431	(61)	GCAGTC	TEGTTTCGCCCAGCGCGTGGAG
Val127-Asn195-Arg426-Gly431	(61)		TTCGTTTCGCCCAGCGCGTGGAG
Val120-Thr202-Ile424-Ala433	(61)		TTCGTTTCGCCCAGCGCGTGGAG
Leu122-Ser199-Arg426-Lys432	(61)		TTEGTTTCGCCCAGCGCGTGGAG
Leu122-Ser199-Arg426-Gly431	(61)		TTCGTTTCGCCCAGCGCCGTGGAG
Lys121-Val200-Asn425-Lys432	(61)		TTCGTTTCGCCCAGCGCGTGGAG
Val120-Ile201-Ile424-Ala433	(61)	Tr. m. 2. brown children	TTCGTTTCGCCCAGCGCCGTGGAG
Val120-Ile201B-Ile424-Ala433	(61)		TTCGTTTCGCCCAGCGCCGTGGAG
Consensus	(61)		TTCGTTTCGCCCAGCGCCGTGGAG
·		91	120
Leu122-Ser199-Tryp427-Gly431	(91)	AAGCTG!	EGGTGACCGTGTACTACGGCGTG
Val127-Asn195-Arg426-Gly431	(91)	AAGCTG!	TGGGTGACCGTGTACTACGGCG <b>TG</b>
Val120-Thr202-Ile424-Ala433	(91)	AAGCIG	GGGTGACCGTGTACTACGGCGTG
Leu122-Ser199-Arg426-Lys <b>432</b>	(91)	<b>AAGCTG</b>	TGGGTGACCGTGTACTACGGCGTG
Leu122-Ser199-Arg426-Gly431	(91)	AAGCTG!	rggctgaccgtgtactacggcg <b>t</b> g
Lys121-Val200-Asn425-Lys432	(91)	AAGCTG	GGGTGACCGTGTACTACGGGGGTG
Val120-Ile201-Ile424-Ala433	(91)	AAGGIG:	regeteaccetetactaceecete
Val120-Ile201B-Ile424-Ala433	(91)	AAGCTGT	FGGGTGACCGTGTACTACGGCGTG
Consensus	(91)	AAGCTGT	TGGGTGACCGTGTACTACGGCGTG
		121	150
Leu122-Ser199-Tryp427-Gly431	(121)	CCCGTGT	TEGAAGGAGGECACCACCCTG
Val127-Asn195-Arg426-Gly431	(121)	CCCGTGI	PGGAAGGAGGCCACCACCACCATG
Val120-Thr202-Ile424-Ala433	(121)	CCCGTGT	rggaaggaggccaccaccacc <b>t</b> g
Leu122-Ser199-Arg426-Lys432	(121)	CCCGTGT	GGAAGGAGGCCACCACCACCGTG
Leu122-Ser199-Arg426-Gly431	(121)	CCCGTGT	GGAAGGAGGCCACCACCACGTG
Lys121-Val200-Asn425-Lys432	(121)		TGGAAGGAGGCCACCACCAGGGTG
Val120-Ile201-Ile424-Ala433	(121)	CCCGTGT	GGAAGGAGGCCACCACCCTG
Val120-Ile201B-Ile424-Ala433	(121)	CCCGTGT	GGAAGGAGGCCACCACCACCTG
Consensus	(121)	CCCGTGT	TGGAAGGAGGCCACCACCCTG
		151	180
Leu122-Ser199-Tryp427-Gly431	(151)	TTCTGCC	CCAGCGACGCCAAGGCCTACGAC
Val127-Asn195-Arg426-Gly431	(151)		CCAGCGACGCCAAGGCCTACGAC
Val120-Thr202-Ile424-Ala433	(151)	TICTGCC	CCAGCGACGCCAAGGCCTACGAC
Leu122-Ser199-Arg426-Lys432	(151)		CCAGCGACGCCAAGGCCTACGAC
Leu122-Ser199-Arg426-Gly431	(151)	TTCTGCC	CCAGCGACGCCAAGGCCTACGAC
Lys121-Val200-Asn425-Lys <b>4</b> 32	(151)	TTCTGCC	CCAGCGACGCCAAGGCCTAGGAC
-			The second secon

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Val120-Ile201-Ile424-Ala433	(151)	TTCTGCGCCAGCGACGCCAAGGCCTACGAC
	(151)	TTCTGCGCCAGCGACGCCAAGGCCTACGAC
Val120-Ile201B-Ile424-Ala433	(151)	TTCTGCGCCAGCGACGCCAAGGCCTACGAC
Conse <b>nsus</b>	(151)	181 210
* 100 0 100 m	/1011	ACCGAGGTGCACAACGTGTGGGCCACCCAC
Leu122-Ser199-Tryp427-Gly431	(181)	ACCGAGGTGCACAACGTGTGGGCCACCCAC
Val127-Asn195-Arg426-Gly431	(181)	ACCGAGGTGCACAACGTGTGGGCCACCCAC
Val120-Thr202-Ile424-Ala433	(181)	
Leu122-Ser199-Arg426-Lys432	(181)	ACCGAGGTGCACAACGTGTGGGCCACCCAC
Leu122-Ser199-Arg426-Gly431	(181)	ACCGAGGTGCACAACGTGTGGGCCACCCAC
Lys121-Val200-Asn425-Lys432	(181)	ACCGAGGTCCACAACGTGTGGGCCACCCAC
Val120-Ile201-Ile424-Ala433	(181)	ACCGAGGTGCACAACGTGTGGGCCACCCAC
Val120-Ile201B-Ile424-Ala433	(181)	ACCGAGGTGCACAACGTGTGGGCCACCCAC
Consensus	(181)	
		211 240
Leu122-Ser199-Tryp427-Gly431	(211)	
Val127-Asn195-Arg426-Gl <b>y43</b> 1	(211)	GCCTGCGTGCCCACCGACCCCAACCCCCAG
Val120-Thr202-Ile424-Ala433	(211)	GCCTGCGTGCCCACCGACCCCAACCCCCAG
Leu122-Ser199-Arg426-Lys432	(211)	GCCTGCGTGCCCACCGACCCCAACCCCCAG
Leu122-Ser199-Arg426-Gly431	(211)	GCCTGGGTGCCCACCGACCCCAACCCCCAG
Lys121-Val200-Asn425-Lys432	(211)	GCCTGCGTGCCCACCGACCCCAACCCCCAG
Val120-Ile201-Ile424-Ala433	(211)	GCTGCGTGCCCACCGACCCCAACCCCCAG
Val120-Ile201B-Ile424-Ala433	(211)	GCCTGCGTGCCCACCGACCCCCAG
Consensus	(211)	
	,	241 270
Leu122-Ser199-Tryp427-Gl <b>y431</b>	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAAC
Val127-Asn195-Arg426-Gly431	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAAC
Val120-Thr202-Ile424-Ala433	(241)	GAGATCCTGCTGGAGAACGTGACCGAGAAC
Leu122-Ser199-Arg426-Lys432	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAAC
Leu122-Ser199-Arg426-Gly431	(241)	GAGATEGTGCTGGAGAACGTGACCGAGAAC
Lys121-Val200-Asn425-Lys432	(241)	GAGATCGTGCTGGGGAGACGTGACCGAGAAC
Val120-Ile201-Ile424-Ala433	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAAC
Val120-Ile201B-Ile424-Ala433	(241)	GAGATEGTGETGGAGAACGTGACCGAGAAC
Consensus	(241)	GAGATCGTGCTGGAGAACGTGACCGAGAAC
C0.10C11045	, ,	271 3.00
Leu122-Ser199-Tryp427-Gly431	(271)	THE ANALYSTIC MAGANCANCATESTIC AG
Val127-Asn195-Arg426-Gly431	(271)	The state of the s
Val120-Thr202-Ile424-Ala433	(271)	TICAACATETGEAAGAAGAACATGGTGGAG
Leu122-Ser199-Arg426-Lys432	(271)	The state of the s
Leu122-Ser199-Arg426-Gly431	(271)	
Lys121-Val200-Asn425-Lys432	(271)	TTCAACATGTGGAAGAACAACATGGTGGAG
Val120-Ile201-Ile424-Ala433	(271)	TTCAACATGTGGAAGAACAACATGGTGGAG
Val120-11e2018-11e424-Ala433	(271)	TTCAACATGTGGAAGAACAACATGGTGGAG
Consensus	(271)	WW
Consensus	(2/1/	301 330
Leu122-Ser199-Tryp427-Gly431	(301)	The state of the s
Val127-Asn195-Arg426-Gly431	(301)	The state of the s
Val120-Thr202-Ile424-Ala433	(301)	The state of the s
Leu122-Ser199-Arg426-Lys432	(301)	
Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431	(301)	CAGATGCACGAGGCATCATCAGCCTGTGG
Lys121-Val200-Asn425-Lys431	(301)	the control of the same of the
Val120-Ile201-Ile424-Ala433		DAGATGCACGAGGACATCATCAGCCTGTGG
		CAGATGCACGAGGACATCATCAGCCTGTGG
Val120-Ile201B-Ile424-Ala433	•	
Consensus	(301)	· · · · · · · · · · · · · · · · · · ·
. 100 0 100 5 407 03 423	12211	The second secon
Leu122-Ser199-Tryp427-Gly431	(331)	
Val127-Asn195-Arg426-Gly431	(331)	
Val120-Thr202-Ile424-Ala433	(331)	GACCAGAGCCTGAAGCCCTGCGTG

•		
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Leu122-Ser199-Arg426-Lys432	(331)	GACCAGAGCCTGAAGCCCTGCGTGAAGCTG
Leu122-Ser199-Arg426-Gly431	(331)	GACCAGAGCCTGAAGCCCTGCGTGAAGCTG
Lys121-Val200-Asn425-Lys432	(331)	GACCAGAGCCTGAAGCCCTGCGTGAA
Val120-Ile201-Ile424-Ala433	(331)	GACCAGAGCCTGAAGCCCTGCGTG
Val120-11e2018-11e424-Ala433	(331)	GACCAGAGCCTGAAGCCCTGCGTG
· • • • • • • • • • • • • • • • • • • •	(331)	A STATE OF THE PROPERTY OF THE
Consensus	(221)	
		361 390
Leu122-Ser199-Tryp427-Gly431	(361)	GG
Val127-Asn195-Arg426-Gly <b>43</b> 1	(361)	ACCCCCTGTGCGTGGGGGCAGGGAACTGC
Val120-Thr202-Ile424-Ala433	(355)	ÇG
Leu122-Ser199-Arg426-Lys432	(361)	GG
Leu122-Ser199-Arg426-Gly431	(361)	GG
Lys121-Val200-Asn425-Lys432	(357)	GG
Val120-Ile201-Ile424-Ala433	(355)	
Val120-Ile201B-Ile424-Ala433	(355)	
Consensus	(361)	GG
Conscious	(551)	391 420
Leu122-Ser199-Tryp427-Gly431	(363)	CAACAGCGTGATCACCCAGGCCTGCCCC
Val127-Asn195-Arg426-Gly431	(391)	AACACCAGCCTGATCACCCAGGCCTGCCCC
		CGGCGCCACCCAGGCCTGCCCC
Val120-Thr202-Ile424-Ala433	(357)	CGCGCGTGATCACCCAGGCCTGCGCCC
Leu122-Ser199-Arg426-Lys432	(363)	CASS at the contraction of the c
Leu122-Ser199-Arg426-Gly431	(363)	caacagegtgatcacccaggectgeccc
Lys121-Val200-Asn425-Lys432	(359)	CCCCEGTGATCACCCAGGCCTGCCCC
Val120-Ile201-Ile424-Ala433	(355)	GEGGGCATCACCCAGGCCTGCCCC
Val120-Ile201B-Ile424-Ala433	(355)	CCCGGCATCACCCAGGCCTGCCCC
Conse <b>nsu</b> s	(391)	CA CAGCGTGATCACCCAGGCCTGCCCC
•		421 450
Leu122-Ser199-Tryp427-Gly431	(391)	AAGGTGAGCTTCGAGCCCATCCCATCCAC
Val127-Asn195-Arg426-Gly431	(421)	AAGGTGAGCTTCGAGCCCATCCAC
Val120-Thr202-Ile424-Ala433	(379)	AAGGTGAGCTTCGAGCCCATCCAC
Leu122-Ser199-Arg426-Lys432	(391)	AAGGTGAGCTTCGAGCCCATCCCCATCCAC
Leu122-Ser199-Arg426-Gly431	(391)	AAGGTGAGCTTCGAGCCCATCCCAC
Lys121-Val200-Asn425-Lys432	(385)	AAGGTGAGCTTCGAGCCCATCCCCCATCCAC
Val120-Ile201-Ile424-Ala433	(379)	
Val120-11e201-11e424-Ala433	(379)	AAGGTGAGCTTEGAGGCCATCCCATCCAC
•		
Consensus	(421)	
Leul22-Ser199-Tryp427-Gly431		NATIGE SERVICES CONTROLL
Val127-Asn195-Arg426-Gly431		TACTGEGECEEGGGGCTTEGCCATECTG
Val120-Thr202-Ile424-Ala433	(409)	
Leu122-Ser199-Arg426-Lys432		TACTEGECC. CEGECGGCTTCGCCATCCTG
Leu122-Ser199-Arg426-Gly431	(421)	TACTGCGCCCCCGGGGCTTCGCCATCCTG
Lys121-Val200-Asn425-Lys432	(415)	TACTOCOCCOCCOCCGCCTTCGCCATCCTG
Val120-Ile201-Ile424-Ala433	(409)	WAR VERGEE RECEGEGED TO GE CAVICE I'G
Val120-Ile201B-Ile424-Ala433		HACHECECCCCCCCCCTTCCCCCATCCTC
Consensus	(451)	
Conscitudo	,/	481 510
Leu122-Ser199-Tryp427-Gly431	(451)	AAGTGCAAGGACAAGAAGTTCAACGGCAGC
Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433	(481)	
vail20-Thr/0/-1164/4-Ala433		
	(439)	the first term of the first of
Leu122-Ser199-Arg426-Lys432	(451)	AAGTGCAACGACAAGAAGTTCAACGGCA <b>G</b> C
Leu122-Ser199-Arg426-Lys <b>432</b> Leu122-Ser199-Arg426-Gl <b>y43</b> 1	(451) (451)	AAGTGCAACGACAAGAAGTTCAACGGCAGC
Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432	(451) (451) (445)	AAGTGCAACGACAAGAAGTTCAACGGCAGC AAGTGCAACGACAAGAAGTTCAACGGCAGC
Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433	(451) (451) (445)	AAGTGCAACGACAAGAAGTTCAACGGCAGC AAGTGCAACGACAAGAAGTTCAACGGCAGC AAGTGCAACGACAAGAAGTTCAACGGCAGC
Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432	(451) (451) (445) (439) (439)	AAGTGCAACGACAAGAAGTTCAACGGCAGC AAGTGCAACGACAAGAAGTTCAACGGCAGC AAGTGCAACGACAAGAAGTTCAACGGCAGC AAGTGCAACGACAAGAAGTTCAACGGCAGC
Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433	(451) (451) (445) (439) (439)	AAGTGCAACGACAAGAAGTTCAACGGCAGC AAGTGCAACGACAAGAAGTTCAACGGCAGC AAGTGCAACGACAAGAAGTTCAACGGCAGC

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Leu122-Ser199-Tryp427-Gly431	(481)	GGCCCCTGCACCA	ACGTGAGCACCGTGCAG
Val127-Asn195-Arg426-Gly431	(511)		ACGTGAGCACCGTGCAG
Val120-Thr202-Ile424-Ala433	(469)	GGCCCCTGCACCA	ACGTGAGCACCGTGC <b>AG</b>
Leu122-Ser199-Arg426-Lys432	(481)		ACGTGAGCACCGTGC <b>AG</b>
Leu122-Ser199-Arg426-Gly431	(481)	GGCCCCTGCACCA	ACGTGAGCACCGTGC <b>AG</b>
Lys121-Val200-Asn425-Lys432	(475)	GGCCCCTGCACCA	ACGTGAGCACCGTGC <b>A</b> G
Val120-Ile201-Ile424-Ala433	(469)	GGCCCCTGCACCA	ACGTGAGCACCGTGC <b>AG</b>
Val120-Ile201B-Ile424-Ala433	(469)	GGCCCCTGCACCA	ACGTGAGCACCGTGC <b>AG</b>
Consensus	(511)	GGCCCCTGCACCA	ACGTGAGCACCGTGCAG
	•	541	570
Leu122-Ser199-Tryp427-Gly431	(511)	TGCACCCACGGCA	TCCCCCCCTGGTGAGC
Val127-Asn195-Arg426-Gly431	(541)		TCCCCCCCGTGGTGAGC
Val120-Thr202-Ile424-Ala433	(499)	TGCACCCACGGCA	TCCGCCCCGTGGTGAGC
Leu122-Ser199-Arg426-Lys432	(511)	TGCACCCACGGCA	TCCGCCCCGTGGTGAGC
Leu122-Ser199-Arg426-Gly431	(511)	TGCACCCACGGCA	TCCGCCCCGTGGTGAGC
Lys121-Val200-Asn425-Lys432	(505)	TGCACCCACGGCA	TCCGCCCCGTGGTGAGC
Val120-Ile201-Ile424-Ala433	(499)	TGCACCCACGGCA	TCCGCCCCGTGGTGÄGC
Val120-Ile201B-Ile424-Ala433	(499)	TGCACCCACGGCA	TCCCCCCGTGGTGAGC
Consensus	(541)		TCCGCCCGTGGTGAGC
0000	,	571	600
Leu122-Ser199-Tryp427-Gly431	(541)	ACCCAGCTGCTGC	TGAACGGCAGCCTGGCC
Val127-Asn195-Arg426-Gly431	(571)		TGAACGGCAGCCTGGCC
Val120-Thr202-Ile424-Ala433	(529)		TGAACGGCAGCCTGGOC
Leu122-Ser199-Arg426-Lys432	(541)		TGAACGCAGCCTGGCC
Leu122-Ser199-Arg426-Gly431	(541)		TGAACGGCAGCCTGGCC
Lys121-Val200-Asn425-Lys432	(535)	ACCCAGCTGCTGC	TGAAGGCAGCCTGGCC
Val120-Ile201-Ile424-Ala433	(529)		TGAACGGCAGCCTGGCC
Val120-Ile201B-Ile424-Ala433	(529)		TGAACGGCAGCCTG <b>GC</b> C
Consensus	(571)	ACCCAGCTGCTGC	TGAACGGCAGCCTGGCC
*		601	630
Leu122-Ser199-Tryp427-Gly431	(571)		TGATCCGCAGCGAGAAC
Val127-Asn195-Arg426-Gly431	(601)	GAGGAGGGCGTGG	TGATCEGCAGEGAGA <b>AC</b>
Val120-Thr202-Ile424-Ala433	(559)	GAGGAGGGCGTGC	tgatecgeagegaga <b>ac</b>
Leu122-Ser199-Arg426-Lys432	(571)		TGATECGCAGCGAGA <b>AC</b>
Leu122-Ser199-Arg426-Gly431	(571)		STGATCCGCAGCGAGA <b>AC</b>
Lys121-Val200-Asn425-Lys432	(565)	GAGGAGGGCGTEC	TGATCEGCAGEGAG <b>AAC</b>
Val120-Ile201-Ile424-Ala433	(559)	GAGGAGGGCGTGC	TGATCCGCAGCGAGAAC
Val120-Ile201B-Ile424-Ala433	(559)		STGATECGCAGCGAGAAC
Consensus	(601)	GAGGAGGGCGTGC	STGATCCGCAGCGAGAAC
		631	660
Leu122-Ser199-Tryp427-Gly431	(601)	TTCACEGACAAC	CCAAGACCATCATCTTG
Val127-Asn195-Arg426-Gly431	(631)	TTCACCGACAACO	CCAAGACCATCATCG <b>T</b> G
Val120-Thr202-Ile424-Ala433	(589)	TTCACCGACAAC	CCAAGACCATCATCG <b>TG</b>
Leu122-Ser199-Arg426-Lys <b>432</b>	(601)	TTEACCGACAAC	CCAAGACCATCATCEIG
Leu122-Ser199-Arg426-Gly431	(601)	THEACCGACAAC	CCAAGACCATCATUG <b>TG</b>
Lys121-Val200-Asn425-Lys432	(595)	TICACGGACAAG	CCAAGACCATGATGG <b>T</b> G
Val120-Ile201-Ile424-Ala433	(589)	TICACCGACAAC	CCAAGACCATCATCG <b>F</b> G
Val120-Ile201B-Ile424-Ala433	(589)		SCCAAGACCATCATCGTG
Consensus	(631)		GCCAAGACCATCATCGTG
		661	690
Leu122-Ser199-Tryp427-Gly431	(631)	CAGCTGAAGGAG	AGCGTGGAGATCAACT <b>G</b> C
Val127-Asn195-Arg426-Gly431		CAGCTGAAGGAG	AGCGTGGAGATCAACT <b>GC</b>
Val120-Thr202-Ile424-Ala433	(619)	CAGCTGAAGGAG	AGCGTGGAGATCAACT <b>GC</b>
Leu122-Ser199-Arg426-Lys432	(631)		AGCGTGGAGATCAAC <b>TGC</b>
Leu122-Ser199-Arg426-Gly431	(631)		AGCGTGGAGATCAACT <b>GC</b>
Lys121-Val200-Asn425-Lys <b>432</b>	(625)		AGCGTGGAGATCAAC <b>TGC</b>
Val120-Ile201-Ile424-Ala433	(619)	CACCIGAAGGAG	AGCGTGGAGATCAACT <b>GC</b>
		*	

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Val12U-11e2U1B-11e424-Ala433	(619)	CAGCTGAAGGAGAGCGTG	AGATCAACTGC
Consensus	(661)	CAGCTGAAGGAGAGCGTGC	
	•	691	720
Leu122-Ser199-Tryp427-Gly431	(661)	ACCCCCCCAACAACAAC	ACCCGCAAGAGC
Val127-Asn195-Arg426-Gly431	(691)	ACCCCCCCAACAACAACA	ACCCGCAAGAGC
Val120-Thr202-Ile424-Ala433	(649)	ACCCCCCCAACAACAAC	NCCCGCAAGAGC
Leu122-Ser199-Arg426-Lys432	(661)	ACCCCCCCAACAACAACA	ACCCGCAAGAGC
Leu122-Ser199-Arg426-Gly431	(661)	ACCEGECCCAACAACAAC	ACCCGCAAGAGC
Lys121-Val200-Asn425-Lys432	(655)	ACCGCCCCAACAACAAC	CCCGCAAGAGC
Val120-Ile201-Ile424-Ala433	(649)	ACCCCCCCAACAACAAC	ACCCGCAAGAGC
Val120-Ile201B-Ile424-Ala433	(649)	ACCCGCCCAACAACAAC	CCCGCAAGAGC
Consensus	(691)		ACCCGCAAGAGC
		721	750
Leu122-Ser199-Tryp427-Gly431	(691)	ATCACCATCGGCCCCGGC	CGCGCCTTCTAC
Val127-Asn195-Arg426-Gly431	(721)	ATCACCATCGGCCCCGGC	
Val120-Thr202-Ile424-Ala433	(679)	ATCACCATCGGCCCCGGC	GCGCCTTGTAC
Leu122-Ser199-Arg426-Lys432	(691)	ATCACCATCGGCCCCGGC	
Leu122-Ser199-Arg426-Gly431	(691)	ATCACCATCGGCCCCGGC	GCGCCTTCT <b>AC</b>
Lys121-Val200-Asn425-Lys432	(685)	ATCACCATCGGCCCCGGC	GCGCCTTCTAC
Val120-Ile201-Ile424-Ala433	(679)	ATCACCATEGGECCCGGC	
Val120-Ile201B-Ile424-Ala433	(679)		
Consensus	(721)	ATCACCATCGGCCCCGGC	CGCGCCTTCTAC
		751	780
Leu122-Ser199-Tryp427-Gl <b>y43</b> 1	(721)	GCCACCGGCGACATCATC	
Val127-Asn195-Arg426-Gly <b>43</b> 1	(751)	GCCACCGGCGACATCATC	
Val120-Thr202-Ile424-Ala433	(709)	GCCACCGGCGACATCATE	
Leu122-Ser199-Arg426-Lys432	(721)	GCCACCGGCGACATCATC	
Leu122-Ser199-Arg426-Gly <b>431</b>	(721)	GCCACCGGCGACATCATC	
Lys121-Va1200-Asn425-Lys <b>432</b>	(715)	GCCACCGGCGACATCATC	
Val120-Ile201-Ile424-Ala433	(709)	GCCACEGGCGACATCATC	
Val120-Ile201B-Ile424-Ala433	(709)	GCCACCGGCGACATCATC	
Consensus	(751)	GCCACCGGCGACATCATC	
•		781	810
Leu122-Ser199-Tryp427-Gly431	(751)	CAGGCCCACTGCAACATC	
Val127-Asn195-Arg426-Gly431	(781)	CAGGCCCACTGCAACATC	AGCGGCGAGAAG
Val120-Thr202-Ile424-Ala433	(739)	CAGGCCCACTGCAACATC	AGCGCEGAGAAG
Leu122-Ser199-Arg426-Lys432	(751)	CAGGCCCAGTGCAACATC	
Leu122-Ser199-Arg426-Gly431	(751)	CAGGCCCACTGCAACATC	
Lys121-Val200-Asn425-Lys432	(745)	CAGGCCGACTGCAACATC	
Val120-Ile201-Ile424-Ala433	(739)	CAGGCCCACTGCAACATC	CCCCCCACAAG
Val120-Ile201B-Ile424-Ala433	(739)	CAGGCCCACTGCAACATC	ACCCCCCACAAC
Consensus	(181)		840
- 100 0 100 m 407 Gl 421	(701)	811 TGGAACAACACCCTGAAG	
Leu122-Ser199-Tryp427-Gly431		The second secon	
Val127-Asn195-Arg426-Gly431	(811)	TGGAACAACACCCTGAAG	
Val120-Thr202-Ile424-Ala433	(769)	TGGAACAACACCCTGAAG	
Leu122-Ser199-Arg426-Lys432	(781) (781)	TGGAACAACACCCTGAAG	
Leu122-Ser199-Arg426-Gly431	(775)	TGGAACAACACCCTGAAG	
Lys121-Val200-Asn425-Lys432			
Vall20-Ile201-Ile424-Ala433 Vall20-Ile201B-Ile424-Ala433	(769) (769)	TGGAACAACACCCTGAAG	
Vall20-lle201B-lle424-Ala433 Consensus	(811)		
Consensus	(011)	841	870
Leu122-Ser199-Tryp427-Gly431	(8111	AAGCTGCAGGCCCAGTTC	
Val127-Asn195-Arg426-Gly431	(841)		
Val127-Ash195-Arg426-Gry451 Val120-Thr202-Ile424-Ala433	(799)	and leading thing have been proper until posterior and a control to	
Leu122-Ser199-Arg426-Lys432		AAGCTGCAGGCCCAGTTC	
menter pertablytidaso_magage	,011/		The second of th

PCT/US99/31272 WO 00/39303 65 33 Leu122-Ser199-Arg426-Gly431 (811) AAGCTGCAGGCCCAGTTCGGCAACAAGACC Lys121-Val200-Asn425-Lys432 (805) AAGCTGCAGGCCCAGTTCGGCAACAAGACC Val120-Ile201-Ile424-Ala433 (799) AAGCTGCAGGCCCAGTTCGGCAACAAGACC Val120-Ile201B-Ile424-Ala433 (799) AAGCTGCAGGCCCAGTTCGGCAACAAGACC Consensus (841) AAGCTGCAGGCCCAGTTCGGCAACAAGACC (841) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC Leu122-Ser199-Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 (871) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC Val120-Thr202-Ile424-Ala433 (829) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC Leu122-Ser199-Arg426-Lys432 (841) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC Leu122-Ser199-Arg426-Gly431 (841) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC (835) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433 (829) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC Val120-Ile201B-Ile424-Ala433 (829) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC Consensus (871) ATCGTGTTCAAGCAGAGCAGCGGCGGCGAC 930 (871) CCCGAGATCGTGATGCACAGCTTCAACTGC Leu122-Ser199-Tryp427-Gly431 (901) CCCGAGATCGTGATGCACAGCTTCAACTGC Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433 (859) CCCGAGATCGTGATGCACAGCTTCAACTGC Leu122-Ser199-Arg426-Lys432 (871) CECGAGATCGTGATGCACAGCTTCAACTGC Leu122-Ser199-Arg426-Gly431 (871) CECGAGATEGTGATGCAEAGETTEAACTGC Lys121-Val200-Asn425-Lys432 (865) CCGGAGATCGTGATGCACAGCTTCAACTGC Val120-Ile201-Ile424-Ala433 CCCGAGATCGTGATGCACAGCTTCAACTGC Val120-Ile201B-Ile424-Ala433 (859) CCCGAGATEGTGATGCACAGCTTCAACTGC Consensus (901) CCCGAGATCGTGATGCACAGCTTCAACTGC Leu122-Ser199-Tryp427-Gly431 (901) GGCGGCGAGTTCTTCTACTGCAACAGCACC Val127-Asn195-Arg426-Gly431 (931) GGCGGCGAGTTCTTCTACTGCAACAGCACC Val120-Thr202-Ile424-Ala433 (889) GGCGGCGAGTTCTTCTACTGCAACAGCACC Leu122-Ser199-Arg426-Lys432 GGCGGCGAGTICTTCTACTGCAACAGCACC Leu122-Ser199-Arg426-Gly431 (901) GGCGGGGAGTTCTTCTACTGCAACAGCACC Lys121-Val200-Asn425-Lys432 (895) GGCGGCGAGTTCTTCTACTGCAACAGCACC Val120-Ile201-Ile424-Ala433 (889)GGCGGCGAGTICETTCTACTGCAACAGCACC Val120-Ile201B-Ile424-Ala433 (889)GGCGGCGAGUI CITICITACIIGCAACAGGACC Consensus (931) GGCGGCGAGTTCTTCTACTGCAACAGCACC Leu122-Ser199-Tryp427-Gly431 (931)CAGCTGTTCAACAGCACCTGGAACAACACC Val127-Asn195-Arg426-Gly431 (961) CAGCTGTTCAACAGGACCTGGAACAACACC Val120-Thr202-Ile424-Ala433 CAGCTGTTCAACAGCACCTGGAACAACACC (919)(931) CAGCTGTTCAACAGGACCTGGAACAACACC Leu122-Ser199-Arg426-Lys432 (931) CAGCTGTTGAACAGCACCTGGAACAACACC Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 (925) CAGCIGITCAACAGCACGIGGAACAACACC Val120-Ile201-Ile424-Ala433 (919) <u>FAGCTGTICAACAGCACCTGGAACAACACC</u> Val120-Ile201B-Ile424-Ala433 (919) CAGCIGITECAACAGCACCIGGAACAACAGC Consensus (961) CAGCTGTTCAACAGCACCTGGAACAACACC 991 1020 Leu122-Ser199-Tryp427-Gly431 (961) AVICEGUECCAA CAACACCAACGGCACCATIC Val127-Asn195-Arg426-Gly431 ATCGGCCCCAACACACCAACGGCACCATC (991)Val120-Thr202-Ile424-Ala433 (949) ATEGGCECEAACAACAGCAACGGCACCATC Leu122-Ser199-Arg426-Lys432 (961) ATCGGCCCCAACAACACCAACGGCACCATC Leu122-Ser199-Arg426-Gly431 (961) ATEGGCCCCAACACACCAACGGCACCATC Lys121-Val200-Asn425-Lys432 (955) ATCGGCCCCAACAACACCAACGGCACGATC

Vall20-Ile201-Ile424-Ala433 (949) ATCGGCCCAACAACACCAACGCACCATC
Vall20-Ile201B-Ile424-Ala433 (949) ATCGGCCCCAACAACACCCAACGCACCATC
Consensus (991) ATCGGCCCCAACAACACCCAACGGCACCATC
1021 1050
Leul22-Serl99-Tryp427-Gly431 (991) ACCCTGCCCTGCCGCATCAAGCAGATCATC

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(1021) ACCCTGCCCTGCCGCATCAAGCAGATCATC
Val127-Asn195-Arg426-Gly431
                               (979) ACCETGECETGCCGCATCAAGCAGATCATC
Val120-Thr202-Ile424-Ala433
                               (991) ACCCTGCCCTGCCGCATCAAGCAGATCATC
Leu122-Ser199-Arg426-Lys432
                               (991) ACCCTGCCCTGCCGCATCAAGCAGATCATC
Leu122-Ser199-Arg426-Gly431
                               (985) ACCCTGCCCTGCCGCATCAAGCAGATCATC
Lys121-Val200-Asn425-Lys432
                               (979) ACCCTGCCCTGCCGCATCAAGCAGATCATC
 Val120-Ile201-Ile424-Ala433
                               (979) ACCCTGCCCTGCCGCATCAAGCAGATCATC
Val120-Ile201B-Ile424-Ala433
                              (1021) ACCCTGCCCTGCCGCATCAAGCAGATCATC
                   Consensus
                              (1021) AACCGCTGGGGCGCAAGGCCATGTACGCC
Leu122-Ser199 Tryp427-Gly431
                              (1051) AACCGCGCGCGCGCAAGGCCATGTACGCC
 Val127-Asn195-Arg426-Gly431
                                     -----GGCGGC---GCCATGTACGCC
 Val120-Thr202-Ile424-Ala433
                              (1009)
                              (1021) MACCGCGCGCGCAACAAGGCCATGTACGCC
 Leu122-Ser199-Arg426-Lys432
                              (1021) AACCGCGCAGCGCAAGGCCATGTACGCC
 Leu122-Ser199-Arg426-Gly431
                              (1015) AAC-----GCCCCCAAGGCCATGTACGCC
 Lys121-Val200-Asn425-Lys432
                              (1009) ------EGCGGC---GCCATGTACGCC
 Val120-Ile201-Ile424-Ala433
                              (1009) ------GGCGGC---GCCATGTACGCC
Val120-Ile201B-Ile424-Ala433
                              (1051) AACCGC G GGCGGCAAGGCCATGTACGCC
                   Consensus
                                                                1110
                               (1051) CCCCCGATCCGCGGCCAGATCCGCTGCAGC
Leu122-Ser199 Tryp427-Gly431
                                     CCCCCATCCGCGGCCAGATCCGCTGCAGC
                               (1081)
 Val127-Asn195-Arg426-Gly431
                                     CCCCCATCCGCGGCCAGATECGCTGCAGC
 Val120-Thr202-Ile424-Ala433
                              (1027)
                                     CCCCCATCCGCGGCCAGATCCGCTGCAGC
 Leu122-Ser199-Arg426-Lys432
                              (1051)
                                     CCCCCATCCGCGGCCAGATCCGCTGCAGC
 Leu122-Ser199-Arg426-Gly431
                               (1051)
                                     CCCCCATCCGCGGCCAGATCCGGTGCAGC
                               (1039)
 Lys121-Val200-Asn425-Lys432
                               (1027) CCCCCCATCCGCGGCCAGATCCGCTGCAGC
 Val120-Ile201-Ile424-Ala433
                               (1027) CCCCCCATCCGCGGCCAGATCCGCTGCAGC
Val120-Ile201B-Ile424-Ala433
                              (1081) CCCCCCATCCGCGGCCAGATCCGCTGCAGC
                   Consensus
                               (1081) AGCAACATCACCGGCCTGCTGACCCGC
Leu122-Ser199 Tryp427-Gly431
                               (1111) AGCAACATGACCGGCCTGCTGCTGACCCGC
 Val127-Asn195-Arg426-Gly431
                               (1057) AGCAACATCACEGGECTGCTGCTGACCEGC
 Val120-Thr202-Ile424-Ala433
                                     AGCAXCATEACCGGCCTGCTGACCCGC
 Leu122-Ser199-Arg426-Lys432
                               (1081)
                                     AGCAACATCACCGGCCTGCTGCTGACCCGC
 Leu122-Ser199-Arg426-Gly431
                               (1081)
                                     ACCAACATCACCGGCCTGCTGCTGACCCGC
 Lys121-Val200-Asn425-Lys432
                               (1069)
                                     ACONAMINACOCCCCINCUICORCANCACOCC
 Val120-Ile201-Ile424-Ala433
                               (1057)
                                     AGGAACAT CAGGGGGCTGGTGCTGAGGCGC
Val120-Ile201B-Ile424-Ala433
                               (1057)
                               (1111) AGCAACATCACCGGCCTGCTGACCCGC
                   Consensus
                               (1111) GAEGGEGEAAGGAGATCAGEAAGAECACC
Leu122-Ser199 Tryp427-Gly431
                                     GACEGEGEAAGGAGATEAGCAACACCACC
 Val127-Asn195-Arg426-Gly431
                               (1141)
                               (1087) GACGGCGCAAGGAGAYCAGCAACACCAGC
 Val120-Thr202-Ile424-Ala433
                               (1111) EACEGCECAAEGAGATCAGCAACACCACC
 Leu122-Ser199-Arg426-Lys432
                               (1111) GAGGCOSCONAGGAGANGAGGAYAGGAGC
 Leu122-Ser199-Arg426-Gly431
                               (1099) GACGGCGGGAAGGAGATCAGCAACACCAGC
 Lys121-Val200-Asn425-Lys432
                               (1087) GAEGGEGGCAAGGAGATEAGCAACAGGAGC
 Val120-Ile201-Ile424-Ala433
                               (1087) GACGGCGGCAAGGAGATCAGCAACACCACC
Val120-Ile201B-Ile424-Ala433
                               (1141) GACGGCGGCAAGGAGATCAGCAACACCACC
                   Consensus
                                                                1200
                                      1171
                                     GAGATOTOCOGCCCGGCGGCGGCGACATG
Leu122-Ser199 Tryp427-Gly431
                               (1141)
                               (1171) GAGATOTTECGCCCGGGGGGGGGGGCGACATG
 Val127-Asn195-Arg426-Gly431
                               (1117) GAGATETTECGCCCCGGCGGCGCGACATG
 Val120-Thr202-Ile424-Ala433
                               (1141) GAGATETTCEGCCCEGGCGGEGGCGACATG
 Leu122-Ser199-Arg426-Lys432
                               (1141) GAGATETTECGCCCCGGCGGEGGEGACATG
 Leu122-Ser199-Arg426-Gly431
                               (1129) GAGATETTEEGECCCGGCGGCGGCGACATG
Lys121-Val200-Asn425-Lys432
                               (1117) GAGATETTEEGECCEGGEGGEGACATG
 Val120-Ile201-Ile424-Ala433
                               (1117) GAGATCTTCCGCCCCGGCGGCGCGCGACATG
Val120-Ile201B-Ile424-Ala433
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		G101@0000000000000000000000000000000000
Consensus	(1171)	GAGATCTTCCGCCCCGGCGCGCGCGACATG
		1201 1230
Leu122-Ser199 Tryp427-Gly431	(1171)	CGCCACAACTEGCCCAGEGAGCTGTACAAG
Val127-Asn195-Arg426-Gly431	(1201)	CGCGACAACTGCCGCGCGGGGCTGTACAA
Val120-Thr202-Ile424-Ala433	(1147)	CGCGACAACTGGCCGCGCGCGGCTGTACAAG
Leu122-Ser199-Arg426-Lys432	(1171)	CGCGACAROGGGGGGGGGGGGGGGGGGGGGGAGG
Leu122-Ser199-Arg426-Gly431	(1171)	CICCACACCUCCCCCACCCACCTCTACACC
Lys121-Val200-Asn425-Lys432	(1159)	CGCGACAACTEGCGCAGCGACCTCTACAAC
Val120-Ile201-Ile424-Ala433	(1147)	CGCCACAACTOGCGCGCGGGGGGGGTGTACAX
Val120-Ile201B-Ile424-Ala433	(1147)	CGCGACAACIGGCGCAGCGAGCTGTACAAG
Consensus	(1201)	CGCGACAACTGGCGCAGCGAGCTGTACAAG
Consensus	(1201)	
I 122 Co == 100 M 427 Cl 421	(1201)	. ====
Leu122-Ser199 Tryp427-Gly431	(1201)	TACAAGGTGGTGAAGATCGAGCCCCTGGGC
Val127-Asn195-Arg426-Gly431	(1231)	TACAAGGTGCTGAAGATCGAGCCCCTGGGC
Val120-Thr202-Ile424-Ala433	(1177)	TACAAGGTGETGAAGATCGAGCCCCTGGGG
Leu122-Ser199-Arg426-Lys432	(1201)	TACAAGGTGGTGAAGATEGAGCCCCTGGGG
Leu122-Ser199-Arg426-Gly431	(1201)	FACAAGGTEGTGAAGATCGAGCCCCTGGGC
Lys121-Val200-Asn425-Lys432	(1189)	TACAAGGTEGTGAAGATCGAGCCCCTGGGC
Val120-Ile201-Ile424-Ala433	(1177)	TACAAGGTGGTGAAGATCGAGCCCCTGGGC
Val120-Ile201B-Ile424-Ala433	(1177)	TACAAGGIGGTGAAGATCGAGCCCCTGGGC
Consensus	(1231)	TACAAGGTGGTGAAGATCGAGCCCCTGGGC
	•	1261 1290
Leu122-Ser199 Tryp427-Gly431	(1231)	GTGGCCCCCCCAAGGCCAAGCGCCGCGTG
Val127-Asn195-Arg426-Gly431	(1261)	GTGGCCCCACCAAGGCCAAGGGCCGCGTG
Val120-Thr202-Ile424-Ala433	(1207)	GTGGGCCCOACCAAGGCCAAGGGCCGCGTG
Leu122-Ser199-Arg426-Lys432	(1231)	GTGGCCCCACCAAGGCCAAGCCCCGCGTG
Leu122-Ser199-Arg426-Gly431	(1231)	
Lys121-Val200-Asn425-Lys432		GTGGCCCCAGCAAGGCCAAGCGCCGCGTG
Vall20-Ile201-Ile424-Ala433	(1219)	GTGGCCCCCACCAAGGCCAAGCGCCGCGTG
	(1207)	GTGGCCCCCACCAAGGCCCAAGCGCCGCGTG
Vall20-Ile201B-Ile424-Ala433	(1207)	GTGGCCCCCACCAAGCCCAAGCCCCGCGTG
		GTGGCCCCACCAAGGCCAAGCGCCGCGTG GTGGCCCCCACCAAGGCCAAGCGCCGCGTG
Vall20-Ile201B-Ile424-Ala433 Consensus	(1207) (1261)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCACCAAGGCCAAGCGCCGCGTG 1291 1320
Vall20-Ile201B-Ile424-Ala433 Consensus Leu122-Ser199 Tryp427-Gly431	(1207)	GTGGCCCCACCAAGGCCAAGCGCGGGTG GTGGCCCCCACCAAGGCCAAGCGCCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGTGACCCTG
Vall20-Ile201B-Ile424-Ala433 Consensus	(1207) (1261)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCACCAAGGCCAAGCGCCGCGTG 1291 1320
Val120-Ile201B-Ile424-Ala433 Consensus Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433	(1207) (1261) (1261)	GTGGCCCCACCAAGGCCAAGCGCGGGTGGTGGTGCCCCACCAAGGCCAAGCGCCGCGTGACAAGCGCGAGAAGCGCGCGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTG
Val120-Ile201B-Ile424-Ala433 Consensus Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431	(1207) (1261) (1261) (1291)	GTGGCCCCACCAAGGCCAAGCGCGGGTGGTGGTGCCCCACCAAGGCCAAGCGCCGCGTGACAAGCGCGAGAAGCGCGCGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTGGTGACCCTG
Val120-Ile201B-Ile424-Ala433 Consensus Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGCGCCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGGCCGTGACCCTG
Vall20-Ile201B-Ile424-Ala433 Consensus  Leu122-Ser199 Tryp427-Gly431 Vall27-Asn195-Arg426-Gly431 Vall20-Thr202-Ile424-Ala433 Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431	(1207) (1261) (1261) (1291) (1237) (1261) (1261)	GTGGCCCCACCAAGGCCAAGGCGGGGGGGGGGGGGGGGG
Val120-Ile201B-Ile424-Ala433 Consensus  Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433 Leu122-Ser199-Arg426-Lys432	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1249)	GTGGCCCCACCAAGGCCAAGGCGGGGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGGGCGTGACCCTG GTGCAGCGCGAGAAGCGGGGCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCGTGACCCTG
Val120-Ile201B-Ile424-Ala433 Consensus  Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433 Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1249) (1237)	GTGGCCCCACCAAGGCCAAGGCGCGCGTG GTGGCCCCCACCAAGGCCAAGCGCGCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGCTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGGGCGCTGACCCTG GTGCAGCGCGAGAAGCGGGGCCGTGACCCTG GTGCAGCGCGAGAAGGGGGCCCTGACCCTG
Val120-Ile201B-Ile424-Ala433 Consensus  Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433 Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1249) (1237) (1237)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG ETGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCAGAAGCGGCGTGACCTG GTGCAGCGCAGAAAGCGCGCGTGACCTG GTGCAGCGCAGAGAAGGGCGCCGTGACCTG GTGCAGCGCAGAGAAGGGCCCCGTGACCTG GTGCAGCGCAGAGAAGGGCCCCGTGACCTG
Val120-Ile201B-Ile424-Ala433 Consensus  Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433 Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1249) (1237)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG ETGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGCGCGTGACCCTG GTGCAGCGCAGAGAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAAGCGCCCGTGACCCTG
Val120-Ile201B-Ile424-Ala433 Consensus  Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433 Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Consensus	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1249) (1237) (1237) (1291)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCCACAAGCGCGCGCTGACCTTG GTGCAGCGCGAGAAGCGCGCGTGACCTTG GTGCAGCGCGAGAAGCGGCGCGTGACCTTG GTGCAGCGCGAGAAGCGGCGCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCTTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTTG GTGCAGCGCGAGAAAGCGCCCCTTGACCTTG GTGCAGCGCGAGAAAGCGCCCCGTGACCCTTG GTGCAGCGCGAGAAAGCGCCCCGTGACCCTTG T321
Val120-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1249) (1237) (1237) (1291)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG ETGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCAGAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCCTGACCCTG GTGCAGCCGCGAGAAGCCCCCTGACCCTG GTGCAGCCGCGAGAAGCCCCCTGACCCTG GTGCAGCCGCGAGAAGCCCCCTGACCCTG GTGCAGCCGCGAGAAGCCCCCTGACCCTG GTGCAGCCCCTGACCCTGCCCCTGACCCTGCCCCTGACCCTGCCCCTGCCCCTGACCCTGCCCCCTGACCCTGCCCCTGCCCCTGACCCTGCCCCTGCCCCTGACCCTGCCCCTGCCCCTGCCCCCTGCCCCCTGCCCCCCCC
Val120-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1321)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCAGAAGCGGCGTGACCCTG GTGCAGCGCAGAAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCGCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCGAGAAGCGCCCGTGACCCTG GTGCAGCGCAGAGAGCGCCCGTGACCCTG GTGCAGCAGAGAGCGCCCGTGACCCTG GTGCAGCAGAGAGCGCCCGTGACCCTG GTGCAGCAGAGAGCGCCCGTGACCCTG GTGCAGCAGAGAGCGCCCGTGACCCTG GTGCAGCAGAGAGCGCCCGTGACCCTG GTGCAGCAGAAGCGCCCGTGACCCTG GTGCAGCAGAGAGCGCCCGTGACCCTG GTGCAGCAGAGAGCGCCCGCCGTGACCCTG GTGCAGCAGAGAGCGCCCGTGACCCTG GTGCAGCAGAGAGCGCCCGCCGCCGCCCCTGACCCTG GTGCAGAGAGCGCCCGCCGCCGCCCCTGACCCTG GTGCAGCAGAGAGCGCCCGCCGCCCCCCCCCC
Val120-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1291) (1321) (1267)	GTGGCCCCACCAAGGCCAAGGCGGGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCAGAAACGCGCGTGACCCTG GTGCAGCGCAGAAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGCGCTGACCCTG GTGCAGCGCAGAAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAAGAAGGGCGCCGTGACCCTG GTGCAGCGAAAAGGGCGCCCGTGACCCTG GTGCAGCGCAAGAAGGGCGCCGTGACCCTG GTGCAGCGCAAGAAGGGCGCCGTGACCCTG GTGCAGCGAAAAGGCGCCCGTGACCCTG GTGCAGCAAGAAGGCGCCCGTGACCCTG GTGCAGCAAGAAGGGCGCCCGTGACCCTG GTGCAGCAAGAAGCGCCCCTGACCCTG GTGCAGCAAGAAGAAGGCGCCCGTGACCCTG GTGCAGCAAGAAGAAGGCGCCCGTGACCCTG GTGCAGCAAGAAGGCGCCCCTGACCCTG GTGCAGCAAGAAGAAGCGCCCCTGACCCTG GTGCAGCAAGAAGAAGCGCCCCTGACCCTG GTGCAGCAAGAAGAAGCGCCCCTGACCCTG GTGCAGCAAGAAGAAGAAGAAGAAAAAGCGCACCCTGAACCCTG GTGCAGCAAAAAGCAAAAAGCAAAAAAAAAA
Val120-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1291) (1291) (1267) (1291)	GTGGCCCCACCAAGGCCAAGGCGGGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCAGAAACCGCGCGTGACCCTG GTGCAGCGCAGAAACCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGGCGTGACCCTG GTGCAGCGCACAAAGCGGCGCTGACCCTG GTGCAGCGCAGAAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAAAAGGGCGCCGTGACCCTG GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCCC GGCGCCATGTTCCTGGGCCCC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1291) (1291) (1291) (1291)	GTGGCCCCACCAAGGCCAAGGCGGGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCAGAAACCGCGCGTGACCCTG GTGCAGCGCAGAAACCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGGCGTGACCCTG GTGCAGCGCACAAAGCGGCGCTGACCCTG GTGCAGCGCAGAAAGCGGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAAGAAGGGCGCCGTGACCCTG GTGCAGCGCAAGAAGGGCGCCGTGACCCTG GGCGCCAAGTTACAGGGCTTCTCGGCGCC GGCGCCAAGTTACAGGGCTTCTCGGCGCC GGCGCCAAGTTACAGGGCTTCTCGGCGCC GGCGCCAAGTTACAGGGCTTCTCGGCGCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCCC GGCGCCAAGTTACAGGGCTTCCTCGGCGCCC GGCGCCAAGTTACAGGCCTTCCTCGGCGCCC GGCGCCAAGTTACAGGCCTTCCTCGGCGCCC GGCGCCAAGTTACAGGCCTTCCTCGGCGCCC GGCGCCAAGTTACAGGCCTTCCTCGCGCCCC GGCGCCAAGTTACAGGCCTTCCTCGCGCCCCCCCCCC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1291) (1267) (1291) (1291) (1279)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCAGAAACCGCGCGTGACCCTG GTGCAGCGCAGAAACCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGGCGTGACCCTG GTGCAGCGCACAAAGCGGCGCTGACCCTG GTGCAGCGCACAAAGCGGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAAAAGGGCGCCGTGACCCTG GTGCAGCGCAAAAGGGCGCCGTGACCCTG GTGCAGCGCAAAAGGGCGCCGTGACCCTG GTGCAGCGCAAAAGGGCGCCGTGACCCTG GTGCAGCGCAAAAGGGCGCCGTGACCCTG GGCGCCAAGTTCCTGGGGCCC GGCGCCAAGTTCCTGGGGCCC GGCGCCAAGTTCCTGGGGCCC GGCGCCAAGTTCCTGGGGCCC GGCGCCAAGTTCCTGGGGGCC GGCGCCAAGTTCCTGGGGGCCC GGCGCCAAGTTCCTGGGGGCCC GGCGCCAAGTTCCTGGGGGCCC GGCGCCAAGTTCCTGGGGGCCC GGCGCCAAGTTCCTGGGGGCCCCGCCC GGCGCCAAGTTCCTGGGCGCCCCCCCCCC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1291) (1291) (1291) (1291) (1279) (1279) (1267)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCAGAAACCGCGCGTGACCCTG GTGCAGCGCAGAAACCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGGCGTGACCCTG GTGCAGCGCACAAAGCGGGCGTGACCCTG GTGCAGCGCACAAAGCGGCCGTGACCCTG GTGCAGCGCAGAAAGGCGCCCGTGACCCTG GTGCAGCGCAGAAAGGCGCCCGTGACCCTG GTGCAGCGCAGAAAGGCGCCCGTGACCCTG GTGCAGCGCAGAAAGGCGCCCGTGACCCTG GTGCAGCGCAGAAAGGCGCCCGTGACCCTG GTGCAGCGCAGAAAGGCGCCCGTGACCCTG GTGCAGCGCAGAAAGGCGCCCGTGACCCTG GTGCAGCGCAAAAGGCGCCCGTGACCCTG GTGCAGCGCAAAAGGCGCCCGTGACCCTG GGCGCCAAGTTCGGGGCCC GGCGCCAAGTTCCGGGGCCC GGCGCCAAGTTCCGGGGCCC GGCGCCAAGTTCCGGGGCCC GGCGCCAAGTTCCGGGGCCC GGCGCCAAGTTCCGGGGCCC GGCGCCAAGTTCCGGGCCCC GGCGCCAAGTTCCGGGGCCC GGCGCCAAGTTCCGGGCCCCCCCCCC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1291) (1267) (1291) (1279) (1267) (1267) (1267)	GTGGCCCCACCAAGGCCAAGGCGGGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCGAGAAGCGCGCGTGACCTG GTGCAGCGCGAGAAGCGCGCGTGACCTG GTGCAGCGCGAGAAGCGGGCGTGACCTG GTGCAGCGCGAGAAGCGGGCGTGACCTG GTGCAGCGCGAGAAGCGGGCGTGACCTG GTGCAGCGCGAGAAGGGGGCCGTGACCTG GTGCAGCGCGAGAAGGGGGCCGTGACCTG GTGCAGCGCGAGAAGGGGCGCGTGACCTG GTGCAGCGCGAGAAGGGGCGCGTGACCTG GTGCAGCGCGAGAAGGGGCGCGTGACCTG GTGCAGCGCGAGAAGGGGCCGTGACCTG GTGCAGCGCGAGAAGGGGCGCCGTGACCTG GTGCAGCGCGAGAAGGGCGCCGTGACCTG GTGCAGCGCGAGAAGGGGCGCCGTGACCTG GTGCAGCGCGAGAAGGGGCGCCGTGACCCTG GTGCAGCGCGAGAAGGGCGCCGTGACCCTG GTGCAGCGCAAGATGCGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGGCTTCCTGGGGGCC GGCGCCATGTTCCTGGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGGCTTCCTGGGCGCC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1237) (1237) (1291) (1291) (1291) (1291) (1291) (1279) (1267) (1267) (1267) (1321)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCCACAAGGCCAGCCGCGTG GTGCAGCGCCACAAGGCCGCGCGCGCACCTG GTGCAGCGCGAGAAGCGCGCGTGACCTG GTGCAGCGCGAGAAGCGGGCGTGACCTG GTGCAGCGCGAGAAAGCGGGCCGTGACCTG GTGCAGCGCGAGAAAGGGGGCCGTGACCTG GTGCAGCGCGAGAAAGGGGGCCGTGACCTG GTGCAGCGCGAGAAAGGGGCCCGTGACCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAGGGGCCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAAGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCCATGTTCCTGGGCCCC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1291) (1291) (1291) (1279) (1279) (1267) (1267) (1321)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCCACAAGGCCAGCGCGCGTG GTGCAGCGCCACAAGGCGCGCGTGACCTTG GTGCAGCGCGAGAAGCGCGCGTGACCTTG GTGCAGCGCGAGAAGCGGGCGTGACCTTG GTGCAGCGCGAGAAAGCGGGCCGTGACCTTG GTGCAGCGCGAGAAAGGGGGCCGTGACCTTG GTGCAGCGCGAGAAAGGGGGCCGTGACCTTG GTGCAGCGCGAGAAAGGGGCCGTGACCTTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAAGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGCCTC GGCGCCCATGTTCCTGGGCCTC GGCGCCCATGTTCCTGGGCCCC GGCGCCCATGTTCCTGGGCCTC GGCGCCCATGTTCCTGGGCCCC GGCGCCCATGTTCCTGGGCCCC GGCGCCCATGTTCCTGGGCCTC GGCGCCCATGTTCCTGGGCCTC GGCGCCCATGTTCCTGGGCCCC GGCGCCCATGTTCCTGGGCCTC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1249) (1237) (1237) (1291) (1291) (1291) (1291) (1291) (1279) (1279) (1267) (1267) (1321)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCCACAAGGCCAGCCGCGTG GTGCAGCGCCACAAGGCCGCGCGCGCACCTG GTGCAGCGCGAGAAGCGCGCGTGACCTG GTGCAGCGCGAGAAGCGGGCGTGACCTG GTGCAGCGCGAGAAAGCGGGCCGTGACCTG GTGCAGCGCGAGAAAGGGGGCCGTGACCTG GTGCAGCGCGAGAAAGGGGGCCGTGACCTG GTGCAGCGCGAGAAAGGGGCCCGTGACCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAGGGGCCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAAGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCATGTTCCTGGGCCCC GGCGCCCATGTTCCTGGGCCCC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1237) (1237) (1291) (1291) (1291) (1267) (1291) (1279) (1267) (1267) (1267) (1321)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCACAAGCGCGCGCTGACCTTG GTGCAGCGCACAAGCGCGCGCGCACCTTG GTGCAGCGCACAAGCGCGCGCGTGACCTTG GTGCAGCGCAGAAAGCGGGCGTGACCTTG GTGCAGCGCAGAAAGCGGGCCGTGACCTTG GTGCAGCGCAGAGAAAGGGGGCCGTGACCTTG GTGCAGCGCAAAAGCGGGCCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCTTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCCCGTGACCCTG GGGCACCACTTCCTGGGCCCC GGCGCCAAGTTCCTGGGCCCC GGCGCCAAGTTCCTGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGCTTCCTTCGGGCGCC GGCGCCATGTTCCTGGGCTTCCTTGGGCGCCC GGCGCCATGTTCCTGGGCTTCCTTCGGGCGCC GGCGCCATGTTCCTGGGCTTCCTTCGGGCGCC GGCGCCATGTTCCTGGGCTTCCTTCGGCCCC GCCGCCATGTTCCTGGGCCCC GCCGCCATGTTCCTGGGCCTTCCTGGGCGCC GCCGCCATGTTCCTGGGCCCC GCCGCCATGTTCCTGGGCCCC GCCCCATGTTCCTGGGCCCC GCCCCATGTTCCTGGGCCCC GCCCCATGTTCCTGGGCCCC GCCCCATGTTCCTGGGCCCC GCCCCATGTTCCTGGGCCCC GCCCCATGTTCCTGGGCCCC GCCCCATGTTCCTGGGCCCC GCCCCATGTTCCTGGCCCCC GCCCCATGTTCCTGGCCCCC GCCCCATGTTCCTGGCCCCC GCCCCATGTTCCTGGCCCCC GCCCCATGTTCCTGGCCCCC GCCCCATGTTCCTGGCCCCC GCCCCATGTTCCTGCCCCCC GCCCCATGTTCCTGCCCCCCCCCC
Vall20-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1237) (1237) (1237) (1291) (1291) (1291) (1291) (1279) (1267) (1267) (1267) (1321) (1321) (1321) (1321) (1351)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCACAAGCGCGCGCTGACCTTG GTGCAGCGCACAAGCGCGCGCGCGACCTTG GTGCAGCGCAGAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGCCGTGACCCTG GTGCAGCGCAGAAAAGCGCGCCGTGACCCTG GTGCAGCGCAGAAAAGCGCGCCGTGACCCTG GTGCAGCGCAGAAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GGCGCCAAGTTCTGGGGCCCCGGGCCCCGGGCCCCGGGCCCCGGGCCCCGGGCCCC
Val120-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1237) (1237) (1237) (1291) (1321) (1267) (1291) (1267) (1267) (1267) (1267) (1321) (1321) (1321) (1351) (1351) (1297)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCACAAGCGCGCGCGCGCGTG GTGCAGCGCGCACAAGCGCGCGCGACCCTG GTGCAGCGCACAAGCGCGCGCGACCCTG GTGCAGCGCACAAGCGCGCGTGACCCTG GTGCAGCGCACAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAAGGGCGCCGTGACCCTG GTGCAGCGCAGAAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GTGCAGCGCGAGAAAGGGCGCCGTGACCCTG GGCGCCATCTTCTGGGCTTCTCGCGCCC GGCGCCATCTTCTGGGCTTCTTCGGCGCC GGCGCCATCTTCTGGGCTTCTTGGCCGC GGCGCCATGTTCTTGGGCTTCCTGGCGCC GGCGCCATGTTCTTGGGCTTCCTGGGCGCC GGCGCCATGTTCCTGGGCTTCCTGGGCGCC GGCGCAGCACAAGGGCCCCCCAGCCTG GCCGCAGCACAAGGGCCCCCCAGCCTG GCCGCAGCACAAGGGCCCCCCAGCCTG GCCGCAGCACAATGGCCCCCCAGCCTG GCCGCAGCACAATGGCCCCCCAGCCTG GCCGCAGCACAATGGCCCCCCCAGCCTG GCCGCAGCACAATGGCCCCCCCAGCCTG GCCGCAGCACAATGGCCCCCCCACCTG
Val120-Ile201B-Ile424-Ala433	(1207) (1261) (1261) (1291) (1237) (1261) (1261) (1237) (1237) (1237) (1291) (1291) (1267) (1291) (1267) (1267) (1267) (1267) (1321) (1321) (1351) (1351) (1321) (1321)	GTGGCCCCACCAAGGCCAAGGCCGCGTG GTGGCCCCACCAAGGCCAAGGCCGCGTG 1291 1320 GTGCAGCGCACAAGCGCGCGCTGACCTTG GTGCAGCGCACAAGCGCGCGCGCGACCTTG GTGCAGCGCAGAAGCGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGCGCGTGACCCTG GTGCAGCGCAGAAAGCGGCCGTGACCCTG GTGCAGCGCAGAAAAGCGCGCCGTGACCCTG GTGCAGCGCAGAAAAGCGCGCCGTGACCCTG GTGCAGCGCAGAAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GTGCAGCGCGAGAAAGCGCGCCGTGACCCTG GGCGCCAAGTTCTGGGGCCCCGGGCCCCGGGCCCCGGGCCCCGGGCCCCGGGCCCC

Lys121-val200-Asn425-Lys432	WO 00/393 <b>03</b>	36 /	65 PCT/US99/3	1272
Val120-11e201-11e424-Ala433   1297    CCCGCARCACATGGCCGCCCCCCCTC Consensus   1351    CCCGCARCACATGGCCGCCCCCCCCCTC Consensus   1351    CCCGCARCACATGGCCGCCCCCCCCCTC Consensus   1351    CCCGCARCACATGGCCGCCCCCACCTG   1361    1410    1410    1417-Asn195-Arq426-G1y431   1351    ACCCTGACCTGCAGCCCCCCACCTG   1361    ACCCTGACCTGCAGCCCCCCACCTG   1361    ACCCTGACCTGCAGCCCCCCACCTGCTG   1361    ACCCTGACCTGCAGCCCCCACCTGCTG   1361    ACCCTGACCTGCAGGCCCCCACCTGCTG   1361    ACCCTGACCTGCAGGCCCCCCACCTGCTG   1361    ACCCTGACCTGCAGGCCCCCACCTGCTG   1361    ACCCTGACCTGCAGGCCCCCACCTGCTG   1361    ACCCTGACCTGAGGCCCCCACCTGCTG   1361    ACCCTGACCTGCAGGCCCCACCACCTG   1361    ACCCTGACCTGCAGGCCCCACCACCTG   1361    ACCCTGACCTGCAGGCCCCACCACCTG   1361    ACCCTGACCTGCAGGCCCCACCACCTG   1361    ACCCTGACCTGCAGGCCCCACCACCTG   1361    ACCCTGACCTGCAGGCCCACCACCTG   1361    ACCCTGACCTGCAGGCCCACCACCTG   1361    ACCCTGACCTGCAGGCCCACCACCTG   1361    ACCCTGACCTGCAGGCCCACCACCTG   1361    ACCCTGACCTGCACCACCACCTG   1361    ACCCTGACCTGCACCACCTG   1361    ACCCTGACCTGCACCACCTG   1361    ACCCTGACCTGCACCACCTG   1361    ACCCTGACCTGCACCACCTG   1361    ACCCTGACCACCTGCACCACCTG   1361    ACCCTGACCACCTGCACCACCTG   1361    ACCCTGACCACCTGCACCACCTG   1361    ACCCTGACCACCTGCACCACCTG   1361    ACCCTGACCACCTGCACCACCTG   1361    ACCCTGACC	Lvs121-Val200-Asn425-Lvs432	(1309)	GCCGCCACCATGGGCGCCCGCAGCCTG	
Val120-Ile201B-Ile424-Ala433   Consensus			The first property of the first property of the section of the first property of the fir	
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1381   1410			to the part of designation and management of the part	
Leu122-Ser199 Tryp427-G1y431	consensus	(1331;		
Val127-Asn195-Arg426-G19431   Val129-Thr202-11e424-Ala433   (1327)   ACCCTGACCGTGCAGCCCGCCAGCTGCTG   Leu122-Ser199-Arg426-G19431   (1351)   ACCCTGACGTGCAGCCCGCCAGCTGCTG   (1351)   ACCCTGACGTGCAGGCCGCCAGCTGCTG   (1351)   ACCCTGACGTGCAGGCCGCCAGCTGCTG   (1351)   ACCCTGACGTGCAGGCCGCCAGCTGCTG   (1351)   ACCCTGACGTGCAGGCCGCCAGCTGCTG   (1351)   ACCCTGACGTGCAGGCCGCCAGCTGCTG   (1351)   ACCCTGACGTGCAGGCCCGCCAGCTGCTG   (1411)   AGCGCGATTGTGCAGCCAGAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAGAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAGCAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGCATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGCATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCGATTGTGCAGCAGCAACAACCTG   (1411)   AGCGCCATTGTGCAGCAGCAC	100122-Sor199 Trup427-Clu431	(1351)		
Val120-Thr202-11e424-Ala433   Leu122-Ser199-Arg426-Gly431   List   ACCCTGACCGTGCAGGCCCGCCAGCTGCTG   Leu122-Ser199-Arg426-Gly431   List   ACCCTGACGGTCCAGGCCCGCCAGCTGCTG   List				
Leu122-Ser199-Arg426-Lys432   (1351)   ACCCTGACCGTCAGGCCCGCAGCTGCTG   Lys121-Val200-Asn425-Lys432   (1351)   ACCCTGACGGTCAGGCCCGCCAGCTGCTG   Lys121-Val200-Asn425-Lys432   (1351)   ACCCTGACGGTCCAGGCCCGCCAGCTGCTG   Val120-Ile201B-Ile424-Ala433   (1327)   ACCCTGACGGTCCAGGCCCGCCAGCTGCTG   (1381)   ACCCTGACGGTCCAGGCCCGCCAGCTGCTG   (1381)   ACCCTGACGGTCCAGGCCCGCCAGCTGCTG   (1381)   ACCCTGACGGTCCAGGCCCGCCAGCTGCTG   (1381)   ACCCTGACGGTCCAGGCCCGCCAGCTGCTG   (1411)   ACCCGGCAGCAGAACAACCTG   (1411)   ACCCGGCATCAGCAGCAGAACAACCTG   (1411)   AGCGGCATCGTCAGCAGCAGAACAACCTG   (1411)   AGCGGCATCGTCAGCAGCAGAACAACCTG   (1411)   AGCGGCATCGTCAGCAGCAGAACAACCTG   (1411)   AGCGGCATCGTCAGCAGCAGAACAACCTG   (1411)   AGCGGCATCGTCAGCAGCAGAACAACCTG   (1411)   AGCGGCATCGTCAGCAGCAGAACAACCTG   (14120-Ile201B-Ile424-Ala433   (1357)   AGCGGCATCGTCAGCAGCAGAACAACCTG   (1411)   AGCGGCATCGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC				
Leu122-Ser199-Arg426-Gly431				
Lys121-Val200-Asn425-Lys432				
Val120-Ile201-Ile424-Ala433				
Val120-Ile201B-Ile424-Ala433   (1327)   ACCCTGACCGTGCAGCCCGCCCGCCAGCTGCTG   ACCCTGACCGTGCAGCCCGCCCGCCAGCCTGCTG   ACCCTGACCGTGCAGCCCGCCCAGCCTGCTG   ACCCTGACCGTGCAGCCAGCCAGCCAGCCAGCCAGCCAGC			15 TO THE PROPERTY AND ADDRESS OF THE PARTY	
Consensus				
1411   1440			The state of the s	
Leu122-Ser199 Tryp427-Gly431	Conse <b>nsus</b>	(1381)		
Val127-Asn195-Arg426-Gly431				
Val120-Thr202-I1e424-Ala433				
Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Lys121-Val201-Asn425-Gly431 Lys121-Val201-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199 Tryp427-Gly431 Leu122-Ser199 Tryp427-Gly431 Val120-Asn425-Lys432 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Leu122-Ser199-Arg426-Gly431 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-Gly431 Val120-Asn425-Lys432 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-Gly431 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-Gly431 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-Gly431 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-I		(1411)	and the second and the second of the second	
Leu122-Ser199-Arg426-G1y431 Lys121-Val200-Asn425-bys432 Val120-Ile2011-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Consensus Consensus  Consensus Val127-Asn195-Arg426-G1y431 Val127-Asn195-Arg426-G1y431 Lys121-Val200-Asn425-bys432 Leu122-Ser199-Arg426-G1y431 Lys121-Val200-Asn425-bys432 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Lys121-Val200-Asn425-bys432 Leu122-Ser199-Arg426-G1y431 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-G1y431 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-G1y431 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-G1y431 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-G1y431 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-G1y431 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-G1y431 Lys121-Val200-Asn425-Lys432 Val120-Ile201B-Ile424-Ala433 V	Val120-Thr202-Ile424-Ala433	(1357)	AGGGGCATEGTGCAGCAGCAGCAACCATG	
Lys121-Val200-Asn425-Lys432	Leu122-Ser199-Arg426-Lys432	(1381)	AGCGGCATCGTGCAGCAGCAGCACCACCTG	
Val120-Ile201-Ile424-Ala433   (1357)   AGCGCATCGTCACCACCACCACACACTG   Val120-Ile201B-Ile424-Ala433   (1357)   AGCGCATCGTGCAGCACCACACACTG   Consensus   (1411)   AGCGCATCGTGCAGCAGCAGCACACACCTG   (1411)   AGCGCCATCGTGCAGCAGCAGCAGCACCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCACGACCACTG   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCCAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCCAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCCAGGCCCAGCACCACCTG   (1411)   CTGCGCGCCATCCAGGCCCAGCACCACCTG   (1411)   CTGCGCGCCATCCAGGCCCAGCACCACCTG   (1411)   CTGCGCGCCATCCAGGCCCAGCACCACCTG   (1411)   CTGCGCGCCATCCAGGCCCAGCACCACCTG   (1411)   CTGCGCGCCATCCAGGCCCAGCACCACCTG   (14120-Ile201-Ile424-Ala433   (1387)   CTGCGCGCCATCCAGGCCCAGCACCACCTG   (14120-Ile201B-Ile424-Ala433   (1387)   CTGCGCGCCATCGAGGCCCAGCACCACCTG   (1411)   CTGCAGCCATCGAGGCCCAGCACCACCTG   (1411)   CTGCAGCCATCGAGGCCCAGCACCACCTG   (1411)   CTGCAGCCATCGAGGCCCAGCACCACCTG   (1411)   CTGCAGCCATCCAGGCCCAGCACCACCTG   (1411)   CTGCAGCCATCCAGGCCCAGCACCACCTG   (1411)   CTGCAGCCATCCAGGCCCAGCACCACCTG   (1411)   CTGCAGCTACCAGGCCCAGCACCACCTG   (1411)   CTGCAGCTACCAGGCCCAGCAGCACCTG   (1411)   CTGCAGCTACCAGGAGCCACCTG   (1411)   CTGCAGCTACCAGGAGCCACCTG   (1411)   CTGCAGCTACCAGGAGCACCTG   (1411)   CTGCAGCTACCAGGAGCACCTGAGCAGCACCTG   (1411)   CTGCAGCTACCAGGAGCACCTGAGCAGCAGCACCTG   (1411)   CTGCAGCTACCAGGAGCACCTGAGCAGCACCTGAGCAGCAGCAGCACCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	Leu122-Ser199-Arg426-Gly431	(1381)	AGCGGCATCGTGCAGCAGCAGCACCACCTG	
Vali20-Ile201B-Ile424-Ala433   (1357)   AGCGGCATGTGCAGCAGCAGCACCTG   Consensus   (1411)   AGCGGCATGTGCAGCAGCAGCACACCTG   1441   1470   1470   Leui22-Seri99 Tryp427-Gly431   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   Vali27-Asni95-Arg426-Gly431   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   Vali20-Thr202-Ile424-Ala433   (1387)   CTGCGGCCATCGAGGCCCAGCAGCACCTG   Ceui22-Seri99-Arg426-Gly431   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCAGCAGCTG   Ceui22-Seri99-Arg426-Gly431   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCAGCAGCTG   Ceui22-Seri99-Arg426-Gly431   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   Vali20-Ile201-Ile424-Ala433   (1387)   CTGCCGCGCATCGAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCACCTG   (1411)   CTGCGCGCCATCGAGGCCCAGCACCTG   (1411)   CTGCAGCTATGCAGGCCCAGCACCACTG   (1411)   CTGCAGCTATGCAGGCCCAGCACCACTG   (1411)   CTGCAGCTATGCAGGCCCAGCACCACTG   (1411)   CTGCAGCTATGCAGGCCCAGCACCACTG   (1411)   CTGCAGCTATGCAGGCCCAGCACCACTG   (1411)   CTGCAGCTATGCAGGCCAGCACCACTG   (1411)   CTGCAGCTATGCAGGCATCAAGCAG   (1411)   CTGCAGCTAGCAGCACCTG   (1411)   CTGCAGCTAGCAGCAGCACCTG   (1411)   CTGCAGCTAGCAGCACCTG   (1411)   CTGCAGCTAGCAGCACCTG   (1411)   CTGCAGCTAGCAGCACCTG   (1411)   CTGCAGCTAGCAGCACCTG   (1411)   CTGCAGCTGACCGTGTGGGCCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGGCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGGCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGGCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGGCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGGCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGCCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGGCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGGCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGCCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGCCATCAAGCAG   (1411)   CTGCAGCTGACCGTGTGGGCCTTGAGGCC   (1411)   CTGCAGCCCGGTGTGGGCCTTGAGGCC   (1411)   CTGCAGCCCGGTGTGGGCCTTGAGGCC   (1411)   CTGCAGCCCG	Lys121-Val200-Asn425-Lys432	(1369)	AGCGGCATCGTGCAGCAGCAGCACCTG	
Consensus		(1357)	AGCGGCATCGTGCAGCAGCAGCAACCTG	
Consensus	Val120-Ile201B-Ile424-Ala433	(1357)	AGCGGCATCGTGCAGCAGCAGCACCTG	
Leu122-Ser199 Tryp427-Gly431	Consensus	(1411)		
Val127-Asn195-Arg426-Gly431			1441 1470	
Val127-Asn195-Arg426-Gly431	Leu122-Ser199 Tryp427-Gly431	(1411)	CTGCGCGCCATCGAGGCCCAGCAGCACCTG	
Val120-Thr202-Ile424-Ala433   (1387)   CTGCGCGCCATCCAGCACCAGCAGCACCTG   Leu122-Ser199-Arg426-Gy431   (1411)   CTGCGCGCCATCCAGGCCCAGCAGCACCTG   Lys121-Val200-Asn425-Lys432   (1399)   CTGCGCGCCATCCAGGCCCAGCAGCACCTG   Val120-Ile201-Ile424-Ala433   (1387)   CTGCGCGCCATCCAGGCCCAGCAGCACCTG   Val120-Ile201B-Ile424-Ala433   (1387)   CTGCGCGCCATCCAGGCCCAGCAGCACCTG   (1441)   CTGCGCGCCATCCAGGCCCAGCAGCACCTG   (1441)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1441)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1441)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1441)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1441)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1441)   CTGCGCGCCATCGAGGCCCAGCAGCACCTG   (1441)   CTGCAGCTGAGCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGAGCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGAGCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGAGCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGAGCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGACCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGACCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGACCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGACCCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGACCCTGTGGGGCATCAAGCAG   (1441)   CTGCAGCTGACCGTGTGGGGCATCAAGCAG   (1441)   CTGCAGCTGACCGTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTGACCGTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTCGCTGTGGGCCATCAAGCAG   (1441)   CTGCAGCTCGCTGTGGGCCTTCAAGCAG   (1441)   CTGCAGCTCGCTGTGGGCCTTCAAGCAG   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (1441)   (				
Leu122-Ser199-Arg426-Lys432 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424				
Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Thr202-Ile424-Ala433 Val120-Thr202-Ile424-Ala433 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Thr202-Ile424-Ala433 Val120-Thr203-Arg426-Gly431 Val120-Thr203-Arg4				
Lys121-Val200-Asn425-Lys432				
Val120-Ile201-Ile424-Ala433         (1387)         CTGCGCGCATCGAGGCCCAGCAGCACCTG           Val120-Ile201B-Ile424-Ala433         (1387)         CTGCGCGCATCGAGGCCCAGCAGCACCTG           Consensus         (1441)         CTGCGCGCATCGAGGCCCAGCAGCACCTG           Leu122-Ser199         Tryp427-Gly431         (1441)         CTGCAGCTATCGAGGCCCAGCAGCACCTG           Val127-Asn195-Arg426-Gly431         (1471)         CTGCAGCTATCGAGGCCCATCAAGCAG           Val120-Thr202-Ile424-Ala433         (1441)         CTGCAGCTATCGAGGCCATCAAGCAG           Leu122-Ser199-Arg426-Gly431         (1441)         CTGCAGCTATCGAGGCCATCAAGCAG           Lys121-Val200-Asn425-Lys432         (1441)         CTGCAGCTGACCGTGTGGGGCATCAAGCAG           Val120-Ile201-Ile424-Ala433         (1417)         CTGCAGCTGACCGTGTGGGGCATCAAGCAG           Val120-Ile201B-Ile424-Ala433         (1417)         CTGCAGCTGACCGTGTGGGGCATCAAGCAG           Val127-Asn195-Arg426-Gly431         (1471)         CTGCAGGTGACCGTGTGGGGCATCAAGCAG           Val120-Thr202-Ile424-Ala433         (1447)         CTGCAGGTGACCGTGTGGGCGTGGACGC           Val120-Thr202-Ile424-Ala433         (1447)         CTGCAGGTCCGTGTGGCCGTGGACGC           Leu122-Ser199-Arg426-Gly431         (1471)         CTGCAGGCCGGTGCTGGCCGTGGACGC           Lys121-Val200-Asn425-Lys432         (1471)         CTGCAGGCCCGGTGCTGGCGTGGACGC           Val120-I				
Val120-Ile201B-Ile424-Ala433	-			
Consensus				
1471   1500				
Consensus	3053545	(		
Val127-Asn195-Arg426-Gly431 (1471)	Leu122-Ser199 Trvp427-Glv431	(1441)		
Val120-Thr202-Ile424-Ala433 (1417) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Leu122-Ser199-Arg426-Cly431 (1441) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Lys121-Val200-Asn425-Lys432 (1429) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Val120-Ile201-Ile424-Ala433 (1417) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Val120-Ile201B-Ile424-Ala433 (1417) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Consensus (1471) CTGCAGCTGACCGTGTGGGGCATCAAGCAG 1501 1530  Leu122-Ser199 Tryp427-Gly431 (1471) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Val120-Thr202-Ile424-Ala433 (1471) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Val120-Thr202-Ile424-Ala433 (1447) CTGCAGGCCGGTGTGGGCGTGAGCGC Leu122-Ser199-Arg426-Cly431 (1471) CTGCAGGCCGGGTGTGGGCGTGAGCGC Lys121-Val200-Asn425-Lys432 (1471) CTGCAGGCCGGGTGTGGGCGTGAGCGC Val120-Ile201-Ile424-Ala433 (1447) CTGCAGGCCGGGTGTGGCGGTGAGCGC Val120-Ile201B-Ile424-Ala433 (1447) CTGCAGGCCGGGTGTGGCCGTGGAGCGC Val120-Ile201B-Ile424-Ala433 (1447) CTGCAGGCCCGGTGGTGGCGGTGAGCGC Consensus (1501) CTGCAGGCCCGGTGGTGGCCGTGAGCGC Val22-Ser199 Tryp427-Gly431 (1501) TACCTGAAGCACCAGCAGCTCCTGGCCATC				
Leu122-Ser199-Arg426-Lys432 (1441) ETGCAGTGAGCGCATCAGCAG Leu122-Ser199-Arg426-Gly431 (1441) CTGCAGCTGACCGTGTGGGGCATCAGCAG Lys121-Val200-Asn425-Lys432 (1429) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Val120-Ile201-Ile424-Ala433 (1417) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Consensus (1471) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Consensus (1471) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Val120-Ser199 Tryp427-Gly431 (1471) CTGCAGCTGACCGTGTGGGGCATCAAGCAG Val120-Thr202-Ile424-Ala433 (1447) CTGCAGGCCGCGTGGGGCGCTGGAGCGC Leu122-Ser199-Arg426-Gly431 (1471) CTGCAGGCCCGCGTGGGGCGCTGGAGCGC Lys121-Val200-Asn425-Lys432 (1471) CTGCAGGCCCGCGTGGGGCGCTGGAGCGC Val120-Ile201-Ile424-Ala433 (1447) CTGCAGGCCCGCGTGGGCGCGCGCCCCGCGCGCGCGCGCG				
Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433 Val120-Ile201B-Ile424-Ala433  Leu122-Ser199 Tryp427-Gly431 Val127-Asn195-Arg426-Gly431 Val120-Thr202-Ile424-Ala433 Leu122-Ser199-Arg426-Lys432 Leu122-Ser199-Arg426-Gly431 Lys121-Val200-Asn425-Lys432 Val120-Ile201B-Ile424-Ala433				
Lys121-Val200-Asn425-Lys432				
Val120-Ile201-Ile424-Ala433       (1417)       ETGCAGCTGACCGTGTGGGGCATCAAGCAG         Val120-Ile201B-Ile424-Ala433       (1417)       ETGCAGCTGACCGTGTGGGGCATCAAGCAG         Consensus       (1471)       CTGCAGCTGACCGTGTGGGGCATCAAGCAG         1501       1530         Leu122-Ser199       Tryp427-Gly431       (1471)       ETGCAGGCCGGGTGCTGGGCGCC         Val127-Asn195-Arg426-Gly431       (1501)       ETGCAGGCCGGGTGCTGGGCGCTGGAGCGC         Val120-Thr202-Ile424-Ala433       (1447)       ETGCAGGCCGGGTGCTGGCCGTGAGCGC         Leu122-Ser199-Arg426-Gly431       (1471)       ETGCAGGCCGGTGCTGGCGTGAGCGC         Lys121-Val200-Asn425-Lys432       (1471)       ETGCAGGCCGGTGCTGGCGTGAGCGC         Val120-Ile201-Ile424-Ala433       (1447)       ETGCAGGCCGGTGCTGGCCGTGGAGCGC         Val120-Ile201B-Ile424-Ala433       (1447)       ETGCAGGCCCGGTGCTGGCCGTGGAGCGC         Val120-Ile201B-Ile424-Ala433       (1447)       ETGCAGGCCCGCGTGCTGGCCGTGGAGCGC         Consensus       (1501)       CTGCAGGCCCGCGTGCTGGCCGTGGAGCGC         1531       1560         Leu122-Ser199       Tryp427-Gly431       (1501)       TACCTGAAGGACCAGCAGCAGCTCCTGGGCATC				
Val120-Ile201B-Ile424-Ala433         (1417)         ETGCAGCTGACCGTGTGGGGCATCAAGCAG           Consensus         (1471)         CTGCAGCTGACCGTGTGGGGCATCAAGCAG           1501         1530           Leu122-Ser199         Tryp427-Gly431         (1471)         ETGCAGGCCGGGTGTGGGCGCTGGAGGGC           Val127-Asn195-Arg426-Gly431         (1501)         CTGCAGGCCGGGTGTGGGCGTGGAGGGC           Val120-Thr202-Ile424-Ala433         (1447)         CTGCAGGCCGGGTGCTGGCGGTGAGGGC           Leu122-Ser199-Arg426-Gly431         (1471)         CTGCAGGCCGGTGCTGGCGGTGAGGGC           Lys121-Val200-Asn425-Lys432         (1471)         CTGCAGGCCGGTGCTGGCGGTGAGGGC           Val120-Ile201-Ile424-Ala433         (1447)         CTGCAGGCCGGTGCTGGCCGTGAGGGC           Val120-Ile201B-Ile424-Ala433         (1447)         CTGCAGGCCCGGTGCTGGCCGTGGAGGGC           Val120-Ser199         Tryp427-Gly431         (1501)         TACCTGAAGGACCAGCAGCTGCTGGGCGTTGGGCGTTGGGCGTTGGCGTTGGGGCGTTGGGGCGTTGGGGCGTTGGGGCGTTGGGGCGTTGGGGCGTTGGGGCGTTGGGGCGTTGGGGGG				
Consensus				
1501   1530   1530   15471   1530   15471   1548   15471   1558	· · · · · · · · · · · · · · · · · · ·			-
Leu122-Ser199 Tryp427-Gly431 (1471) CTGCAGGCCGGGTGTGGGCGTGGAGGGC Val127-Asn195-Arg426-Gly431 (1501) CTGCAGGCCGGTGTGGGCGTGGAGGGC Val120-Thr202-Ile424-Ala433 (1447) CTGCAGGCCGGTGTGGGCGTTGGAGGGC Leu122-Ser199-Arg426-Cly431 (1471) CTGCAGGCCGGTGTGGGCGTGGAGGGC Lys121-Val200-Asn425-Lys432 (1471) CTGCAGGCCGGTGTGGCGGTGGAGGGC Val120-Ile201-Ile424-Ala433 (1447) CTGCAGGCCGGGGGCGTGGAGGGC Val120-Ile201B-Ile424-Ala433 (1447) CTGCAGGCCGGGGGGGGGGGGGGC Consensus (1501) CTGCAGGCCCGGTGGCGGTGGAGGGC Leu122-Ser199 Tryp427-Gly431 (1501) TACCTGAAGGACCAGCAGCTGCTGGCGTTG	00.000.00		· ·	
Val127-Asn195-Arg426-Gly431       (1501)       CTGCAGGCCGGTGTGGGCGTGGAGGGC         Val120-Thr202-Ile424-Ala433       (1447)       CTGCAGGCCGGTGTGGGCGTGGAGGGC         Leu122-Ser199-Arg426-Lys432       (1471)       CTGCAGGCCGGTGCTGGCCGTGAGGGC         Leu122-Ser199-Arg426-Gly431       (1471)       CTGCAGGCCGGGTGCTGGCCGTGAGGGC         Lys121-Val200-Asn425-Lys432       (1459)       CTGCAGGCCGGGTGCTGGCCGTGAGGGC         Val120-Ile201-Ile424-Ala433       (1447)       CTGCAGGCCCGGTGCTGGCCGTGAGGGC         Val120-Ile201B-Ile424-Ala433       (1447)       CTGCAGGCCCGGTGCTGGCCGTGAGGGC         Consensus       (1501)       CTGCAGGCCCGGTGCTGGCCGTGGAGGGC         Leu122-Ser199       Tryp427-Gly431       (1501)       TACCTGAAGGACCAGCAGCTGCTGGGCATC	Leu122-Ser199 Trvn427-Glv431			
Vall20-Thr202-Ile424-Ala433 (1447) CTGCAGGCCGCGTGTGGCCGTGAGGGC Leu122-Ser199-Arg426-Lys432 (1471) CTGCAGGCCGCGTGTGGCCGTGAGGGC Leu122-Ser199-Arg426-Gly431 (1471) ETGCAGGCCGGCGTGTGGGCGTGGAGGGC Lys121-Val200-Asn425-Lys432 (1459) CTGCAGGCCGCGTGTGGCCGTGGAGGGC Vall20-Ile201-Ile424-Ala433 (1447) CTGCAGGCCGGGGCGTGGAGGGC Val120-Ile201B-Ile424-Ala433 (1447) CTGCAGGCCGGGGGGGGGGGGGGGGC Consensus (1501) CTGCAGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
Leu122-Ser199-Arg426-Lys432 (1471) CTGCAGGCCGGTGTGGCCGTGGAGGGC Leu122-Ser199-Arg426-Gly431 (1471) ETGCAGGCCGGGTGTGGGCGTGGAGGGC Lys121-Val200-Asn425-Lys432 (1459) CTGCAGGCCGGTGTGGGCGTGGAGGGC Val120-Ile201-Ile424-Ala433 (1447) CTGCAGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
Leu122-Ser199-Arg426-Gly431 (1471) ETGCAGGCCCGCTGCGCGCTGGAGGCC Lys121-Val200-Asn425-Lys432 (1459) ETGCAGGCCCGCTGCTGGCCGTGGAGGCC Val120-Ile201-Ile424-Ala433 (1447) ETGCAGGCCCGCGTGCTGGCCGTGGAGGGC Val120-Ile201B-Ile424-Ala433 (1447) ETGCAGGCCCGTGGCCGTGGAGGGC Consensus (1501) CTGCAGGCCCGCTGGCCGTGGAGGGC 1531 1560 Leu122-Ser199 Tryp427-Gly431 (1501) TACCTGAAGGACCAGCAGCTGCTGGGCATC				
Lys121-Val200-Asn425-Lys432 (1459) CTGCAGGCCGCGTGCTGGAGGGC Val120-Ile201-Ile424-Ala433 (1447) CTGCAGGCCGCGTGCTGGCGTGGAGGGC Val120-Ile201B-Ile424-Ala433 (1447) CTGCAGGCCGGTGCTGGCCGTGGAGGGC Consensus (1501) CTGCAGGCCCGGTGCTGGCCGTGGAGGGC 1531 1560 Leu122-Ser199 Tryp427-Gly431 (1501) TACCTGAAGGACCAGCAGCTGCTGGGCATC				
Val120-Ile201-Ile424-Ala433 (1447) CTGCAGGCCGGGGGGGGGGGGCCCGGGGGGGGGGGGGGG				
Vall20-Ile201B-Ile424-Ala433 (1447) CTGCAGGCCEGCGTGCGGGGGGCCCCGCGTGCAGCGCCCGCGTGCAGCGCCCGCGTGCAGCGCCCGCGTGCAGCGCCCGCGTGCAGCGCCCGCGTGCAGCGCCCGCGGGCGCCCCCGCGCAGCAGCAGCAGCAGC				
Consensus (1501) CTGCAGGCCGCGTGCTGGAGCGC 1531 1560 Leu122-Ser199 Tryp427-Gly431 (1501) TAGCTGAAGGACCAGCAGCTGCTGGGCATC				
1531 1560 Leul22-Ser199 Tryp427-Gly431 (1501) TACCTGAAGGACCAGCAGCTGCTGGGCATC	the state of the s		A CONTRACTOR OF THE PROPERTY O	
Leu122-Ser199 Tryp427-Gly431 (1501) TACCTGAAGGACCAGCAGCTGCTGGGCATC	Consensus		•	•
	1 au 1 2 2 Caw 1 0 0 m 4 2 7 C1 4 2 1			
Valiz/-Ashiss-Argazo-Giyasi (1551) [ACCTGANGCACCAGCAGCTGGGGGATC				
	val127-A511133-AEG426-G19431	(1931)	A ACE TORAGO ACCASCA TO THE TORAGO ATC	

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(1477) TACCTGAAGGACCAGCAGCTGCTGGGCATC
 Val120-Thr202-Ile424-Ala433
                                      TACCTGAAGGACCAGCAGCTGCTGGGCATC
 Leu122-Ser199-Arg426-Lys432
 Leu122-Ser199-Arg426-Gly431
                                      TACCTGAAGGACCAGCAGCTGCTGGGCATC
                               (1501)
                                      TACCTGAAGGACCAGCAGCTGCTGGGCATC
                               (1489)
 Lys121-Val200-Asn425-Lys432
                                      TACCTGAAGGACCAGCAGCTGCTGGGCATO
 Val120-Ile201-Ile424-Ala433
                               (1477)
                                      TACCTGAAGGACCAGCAGCTGCTGGGCATC
Val120-Ile201B-Ile424-Ala433
                               (1477)
                               (1531) TACCTGAAGGACCAGCAGCTGCTGGGCATC
                   Consensus
                                      TGGGGCTGCAGGGGGAAGCTGATCTGCAGG
                               (1531)
Leu122-Ser199 Tryp427-Gly431
                                      TGGGGCTGCAGCGG@AAGCTGATCTGCACC
                               (1561)
 Val127-Asn195-Arg426-Gly431
                                      TGGGGCTGCAGCGKGAAGCTGATCTGCACC
                               (1507)
 Val120-Thr202-Ile424-Ala433
                                      TGGGGCTGCAGCGGCAAGCTGATCTGCACC
                               (1531)
 Leu122-Ser199-Arg426-Lys432
 Leu122-Ser199-Arg426-Gly431
                               (1531)
                                      TGGGGCTGCAGCGGCAAGCTGATCTGCACC
                                      TGGGGCTGCAGGGGCAAGCTGATCTGCACC
                               (1519)
 Lys121-Val200-Asn425-Lys432
                                      TGGGGCTGCAGCGGCAAGCTGATCTGCACC
                               (1507)
 Val120-Ile201-Ile424-Ala433
                                      TGGGGCTGCAGCGGCAAGCTGATCTGCACC
Val120-Ile201B-Ile424-Ala433
                               (1507)
                                      TGGGGCTGCAGCGGCAAGCTGATCTGCACC
                    Consensus
                               (1561)
                               (1561) ACCGCCTGCCCTGGAACGCCAGCTGGAGC
Leu122-Ser199 Tryp427-Gly431
                                      ACCGCCGTGCCCTGGAGC
 Val127-Asn195-Arg426-Gly431
                               (1591)
                                      ACCGCGGTGCCCTGGAACGCCAGCTGGAGC
 Val120-Thr202-Ile424-Ala433
                               (1537)
                                      ACCGCCGTGCCCTGGAACGCCAGCTGGAGC
 Leu122-Ser199-Arg426-Lys432
                               (1561)
                                      ACCGCCGTGCCCTGGAACGCCAGCTGGAGC
 Leu122-Ser199-Arg426-Gly431
                               (1561)
                                      ACCCCCTGCCTGCAACCCCAGETGGAGC
                               (1549)
 Lys121-Val200-Asn425-Lys432
                                      ACCGCCGTGCCCTGGAACGCCAGCTGGAGC
 Val120-Ile201-Ile424-Ala433
                               (1537)
Val120-Ile201B-Ile424-Ala433
                               (1537)
                                      ACCGCCGTGCCCTGGAACGCCAGCTGGAGC
                               (1591) ACCGCCGTGCCCTGGAACGCCAGCTGGAGC
                    Consensus
                                      1621
                                                                 1650
                               (1591) AACAAGAGCCTGGACCAGATCTGGAACAAC
Leu122-Ser199 Tryp427-Gly431
 Val127-Asn195-Arg426-Gly431
                                      AACAAGAGCCTGGAGCAGATCTGGAACAAC
                               (1621)
                                      AACAAGAGCCTEGACCAGATCTGGAACAAC
 Val120-Thr202-Ile424-Ala433
                               (1567)
                               (1591) AACAAGAGCCTGGACCAGATCTGGAACAAC
 Leu122-Ser199-Arg426-Lys432
                               (1591) · AACAAGAGCCTGCACCAGATCTGGAACAAC
 Leu122-Ser199-Arg426-Gly431
                                      AACAAGAGCCTGGACCAGATCTGGAACAAC
 Lys121-Val200-Asn425-Lys432
                               (1579)
                                      RACAAGAGCETGGACCAGATCTGGAACAAC
 Val120-Ile201-Ile424-Ala433
                               (1567)
                                      AACAAGAGCCTGGACCAGATCTGGAACA<mark>AC</mark>
Val120-Ile201B-Ile424-Ala433
                               (1567)
                               (1621) AACAAGAGCCTGGACCAGATCTGGAACAAC
                    Consensus
                               (1621) ATGACCTGGATGGAGTGGGAGCGCGAGATC
Leu122-Ser199 Tryp427-Gly431
                               (1651) ATGACCTGGATGGAGTGGGAGGGGGAGATC
 Val127-Asn195-Arg426-Gly431
                                      ATGACCTGGATGGAGTGGGAGEGCGAGATC
 Val120-Thr202-Ile424-Ala433
                               (1597)
                               (1621) ATGACCIGGATGGAGTGGGGGGGGGGGGGAGATC
 Leu122-Ser199-Arg426-Lys432
                                      ATGACCTGGATGGAGTGGGAGCGCGAGATC
 Leu122-Ser199-Arg426-Gly431
                               (1621)
                               (1609) ATGACITGGATGGAGTGGAGCGCGAGATE
 Lys121-Val200-Asn425-Lys432
                                      ATGACCTIGGATIGGAGTEGGAGCGCGAGATE
                               (1597)
 Val120-Ile201-Ile424-Ala433
                               (1597) ATGACCTGGATGSAGTGGGAGCGCGAGATC
Val120-Ile201B-Ile424-Ala433
                               (1651) ATGACCTGGATGGAGTGGGAGCGCGAGATC
                    Consensus
                                                                 1710
                               (1651) GACAACTACACCAACCTGATCTACACCCTG
Leu122-Ser199 Tryp427-Gly431
                               (1681). GACAACTACACCAACCTGATCTACACCCTG
 Val127-Asn195-Arg426-Gly431
                               (1627) GACAACTAGACCAACCTGATGLACACCCTG
 Val120-Thr202-Ile424-Ala433
 Leu122-Ser199-Arg426-Lys432
                               (1651) GACAACTACACCAACCTGATCTACACCCTG
                               (1651) GACAACTACACCAACCTGAICTACACCCTG
 Leu122-Ser199-Arg426-Gly431
                               (1639) GACAACTACACGAACCTGATCTACACCCTG
 Lys121-Val200-Asn425-Lys432
                                      EACAACTACACCANCETGATCTACACCCTG
                               (1627)
 Val120-Ile201-Ile424-Ala433
                                      GACAACTACACCAACCTGATCTACACCCTG
                               (1627)
Val120-Ile201B-Ile424-Ala433
                               (1681) GACAACTACACCAACCTGATCTACACCCTG
                    Consensus
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		1711	1740
Leu122-Ser199 Tryp427-Gly431	(1681)		agaaccagcaggag <b>aa</b> g
Val127-Asn195-Arg426-Gly431	(1711)		AGAACCAGCAGGAGAAG
Val120-Thr202-Ile424-Ala433	(1657)		AGAACCAGCAGGAGAAG
Leu122-Ser199-Arg426-Lys432	(1681)		AGAACCAGCAGGAGAAG
Leu122-Ser199-Arg426-Gl <b>y43</b> 1	(1681)		agaaccagcagaga <b>a</b> g
Lys121-Val200-Asn425-Lys432	(1669)		AGAACCAGCAGGAGAAG
Val120-Ile201-Ile424-Ala433	(1657)		agaaccagcagcaga <b>a</b> g
Val120-Ile201B-Ile424-Ala433	(1657)		AGAACCAGCAGAGAAG
Consensus	(1711)		AGAACCAGCAGGAGAAG
		1741	1770
Leu122-Ser199 Tryp427-Gly431	(1711)		IGCTGGAGCTGGACAAG
Val127-Asn195-Arg426-Gly431	(1741)		IGCTGGAGCTGGACA <b>AG</b>
Val120-Thr202-Ile424-Ala433	(1687)		IGCTGGAGCTGGACAAG
Leu122-Ser199-Arg426-Lys432	(1711)		TGCTGGAGCTGGACAAG
Leu122-Ser199-Arg426-Gly431	(1711)		IGCTGGAGCTGGACAAG
Lys121-Val200-Asn425-Lys432	(1699)		TGCTGGAGCTGGAGAAG
Val120-Ile201-Ile424-Ala433	(1687)		igctggagctggag <b>aa</b> g
Val120-Ile201B-Ile424-Ala433	(1687)		IGCTGGÄGCTGGÄGAAG
Consensus	(1741)		TGCTGGAGCTGGACAAG
		1771	1800
Leu122-Ser199 Tryp427-Gly431	(1741)		SGAACTGGTTCGACATC
Val127-Asn195-Arg426-Gly431	(1771)	A STATE OF THE PARTY OF THE PAR	GGAACTGGTTCGACATC
Val120-Thr202-Ile424-Ala433	(1717)		GGAACTGGTTCGACATC
Leu122-Ser199-Arg426-Lys432	(1741)		GGACTGGTTCGACATC
Leu122-Ser199-Arg426-Gly431	(1741)		SGAACTGGTTCGACATC
Lys121-Val200-Asn425-Lys432	(1729)		GAACTGGTTCGACATC
Val120-Ile201-Ile424-Ala433	(1717)		GGAACTGGTTCGACATC GGAACTGGTTCGACATC
Vall20-Ile201B-Ile424-Ala433	(1717)		GGAACTGGTTCGACATC
Consensus	(1771)	1801	1830
Leu122-Ser199 Tryp427-Gly431	(1771)		GTACATCAAGATCTTC
Val127-Asn195-Arg426-Gly431	(1801)		GTACATCAAGATCETC
Val120-Thr202-Ile424-Ala433	(1747)		GTACATCAAGATCETT
Leu122-Ser199-Arg426-Lys432	(1771)		GEVACAR <b>C</b> AAGAREVEY <b>C</b>
Leu122-Ser199-Arg426-Gly431	(1771)		SETVACATIONA CLAVICIUM
Lys121-Val200-Asn425-Lys432	(1759)	ACCANGUCECTOR	CTACATONACATOTTC
Val120-Ile201-Ile424-Ala433	(1747)		GTACATCAAGATCITC
Val120-Ile201B-Ile424-Ala433			GTACATCAAGATCITC
Consensus			GTACATCAAGATCTTC
331133113	(	1831	1860
Leu122-Ser199 Tryp427-Gly431	(1801)	ATCATGATCGTGG	EEGGGTGGTGGGGGGTG
Val127-Asn195-Arg426-Gly431	(1831)		SCGCCTGGTGGGCCTG
Val120-Thr202-Ile424-Ala433			COGCCTGGTCGGCCTC
Leu122-Ser199-Arg426-Lys432			eggeotigetigegeo <b>tig</b>
Leu122-Ser199-Arg426-Gly431	(1801)	ATCATGATEGTEG	SCGGCCTGGTGGGCCTTG
Lys121-Val200-Asn425-Lys432	(1789)	ATCATGATCGTGG	CEECCIEETEECCCIE
Val120-Ile201-Ile424-Ala433	(1777)	ATCATGATCGTGG	GEGECTEETEGECETE
Val120-Ile201B-Ile424-Ala433	(1777)	ATCAVIGATICGTEG	eeccontectedecic
Consensus	(1831)		CCGCCTGGTGGGCCTG
		1861	1890
Leu122-Ser199 Tryp427-Gly431			CCTGCTGAGCATCGTG
Val127-Asn195-Arg426-Gly431	(1861)		CGTGCTGAGCATCG <b>TG</b>
Val120-Thr202-Ile424-Ala433	(1807)		CGTGCTGAGCATCGTG
Leu122-Ser199-Arg426-Lys432	(1831)		ECGTGCTGAGCATEG <b>T</b> G
Leu122-Ser199-Arg426-Gly431	(1831)		CGTGCTGAGCATEGTG
Lys121-Val200-Asn425-Lys432	(1819)	EGCATEGTGTTCA(	CGTGCTGAGCATCGTG

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(1807) CGCATCGTGTTCACCGTGCTGAGCATCGTG
     Val120-Ile201-Ile424-Ala433
   Val120-Ile201B-Ile424-Ala433
                                                       (1807) CGCATCGTGTTCACCGTGCTGAGCATCGTG
                                                       (1861) CGCATCGTGTTCACCGTGCTGAGCATCGTG
                                    Consensus
   Leu122-Ser199 Tryp427-Gly431
                                                       (1861) AACCGCGTGCGCCAGGGCTACAGCCCCCTG
                                                       (1891) AACCGCGTGCGCCAGGGCTACAGCGCCCTG
     Val127-Asn195-Arg426-Gly431
     Val120-Thr202-Ile424-Ala433
                                                       (1837) AACCGCGTGCGCCAGGGCTACAGCCCCCTG
     Leu122-Ser199-Arg426-Lys432
                                                       (1861) AACEGEGTEEGCCAGGGCTACAGCCCCCTG
     Leu122-Ser199-Arg426-Gly431
                                                       (1861) AACEGEGTEEGECAGGGCTACAGCCCCCTG
    Lys121-Val200-Asn425-Lys432
                                                                  AACEGCGTGEGCEAGGGCTACAGCCCCCTG
                                                       (1849)
     Val120-Ile201-Ile424-Ala433
                                                       (1837)
                                                                  AACCGCGTGGGCCAGGGCTACAGCCCCCTG
   Val120-Ile201B-Ile424-Ala433
                                                                  AACCGCGTGCGCCAGGGCTACAGCCCCCTG
                                                       (1837)
                                   Consensus
                                                       (1891) AACCGCGTGCGCCAGGGCTACAGCCCCCTG
  Leu122-Ser199 Tryp427-Gly431
                                                      (1891) AGCTTCCAGACCCGCTTCCCCGCCCCCGC
                                                      (1921) AGETTECAGACCEGETTECCEGECECECGC
    Val127-Asn195-Arg426-Gly431
    Val120-Thr202-Ile424-Ala433
                                                      (1867) AGETTCCAGACCCGCTTCCCCGCCCCCGC
    Leu122-Ser199-Arg426-Lys432
                                                      (1891) AGCTTCCAGACCCGCTTCCCCGCCCCCGC
    Leu122-Ser199-Arg426-Gly431
                                                      (1891) AGETTECAGACEGGCTTCGCCGGCCCCGGC
    Lys121-Val200-Asn425-Lys432
                                                      (1879) AGCITICCAGACCCGCTTECCCGCCCCCCCC
    Val120-Ile201-Ile424-Ala433
                                                      (1867) AGCTTCCAGACCCGCTTCCGCGCCCCCGC
  Val120-Ile201B-Ile424-Ala433
                                                                 AGCITTECAGACCCCGTTTCCCCGGGGGGGGGGCGC
                                                      (1867)
                                                      (1921) AGCTTCCAGACCCGCTTCCCCGCCCCCCGC
                                   Consensus
                                                                  1951
  Leu122-Ser199 Tryp427-Gly431
                                                                 (1921)
    Val127-Asn195-Arg426-Gly431
                                                      (1951) GGCCCCGACGGCCCCGAGGCCATCGAGGAG
                                                                 GGCCCCGACCGCCGAGGGCATCGAGGAG
    Val120-Thr202-Ile424-Ala433
                                                      (1897)
   Leu122-Ser199-Arg426-Lys432
                                                      (1921)
                                                                 GGCCCCGACCGCCCCGAGGGCATCGAGGAG
   Leu122-Ser199-Arg426-Gly431
                                                                 GGeeccheesecograggeaucgaggag
   Lys121-Val200-Asn425-Lys432
                                                                 <u>ecoegramment errectvoster akoleveture</u>
                                                      (1909)
                                                                 CORNECT CALLER COVER OF PARTY AND COVER OF THE COVER OF T
   Val120-Ile201-Ile424-Ala433
                                                     (1897)
  Val120-Ile201B-Ile424-Ala433
                                                                 ECGOVECACEOS GOCACCOAMEGACOA
                                                     (1897)
                                  Consensus
                                                     (1951) GGCCCCGACCGCCCCGAGGGCATCGAGGAG
                                                                                                              2010
 Leu122-Ser199 Tryp427-Gly431
                                                     (1951) GAGGGGGGGGAGGGGGAGGGGAGG
                                                                 GAGGGGGGGAGGGGAGGGGAGC
   Val127-Asn195-Arg426-Gly431
                                                                 GAGGGGGGGAGGGGACCGZGACCGCAGC
   Val120-Thr202-Ile424-Ala433
                                                     (1927)
                                                                 Leu122-Ser199-Arg426-Lys432
                                                     (1951)
   Leu122-Ser199-Arg426-Gly431
                                                                 द्वाश्चद्यत्त्रव्यक्षस्यम् यस्य स्थानस्य स्थानस्य स्थानस्य स्थानस्य स्थानस्य स्थानस्य स्थानस्य स्थानस्य स्थानस्
                                                     (1951)
   Lys121-Val200-Asn425-Lys432
                                                                 <u>ଜ୍ୟପ୍ରସ୍ଥରଣ୍ଟର୍ଜ୍ୟ ପ୍ରସ୍ଥର୍ଟ୍ର କ୍ୟୁଟ୍ର ପ୍ରଥମ ଅନ୍ୟୁଟ୍ର ପ୍ରଥମ ଅନ୍ୟୁଟ୍ର ପ୍ରଥମ ଅନ୍ୟୁଟ୍ର ପ୍ରଥମ ଅନ୍ୟୁଟ୍ର ପ୍ରଥମ ଅନ୍ୟୁ</u>
                                                     (1939)
   Val120-Ile201-Ile424-Ala433
                                                                 द्यम्बत्तव्यव्यवस्थाः । त्राप्तव्यवस्थाः । त्राप्तवस्थाः । त्राप्तवस्थाः । त्राप्तवस्थाः । त्राप्तवस्थाः । त्र
                                                     (1927)
 Val120-Ile201B-Ile424-Ala433
                                                     Consensus
                                                     (1981) GAGGGCGGCGACCGCGACCGCAGC
                                                                                                              2040
                                                     (1981) Демесентентен кесемпестисементе
 Leu122-Ser199 Tryp427-Gly431
   Val127-Asn195-Arg426-Gly431
                                                     (2011) AGESCOTIGNIGO AGGS PROPERSON CON
   Val120-Thr202-Ile424-Ala433
                                                     (1957)
                                                                AGCCOCCRECTED ACCCCC CERCCCCCC
                                                     (1981) AGCCCCCTGGTGCACGGCCTGCTGGCCCTG
  Leu122-Ser199-Arg426-Lys432
  Leu122-Ser199-Arg426-Gly431
                                                     (1981) AGCCCCTESTECACGCCCTEGTEGCCCTE
  Lys121-Val200-Asn425-Lys432
                                                     (1969) AGECECTESTECACGECTECTGECCETG
  Val120-Ile201-Ile424-Ala433
                                                     (1957) AGGCCCCTGGTGCACGGCGTGCTGGGCCCTG
 Val120-Ile201B-Ile424-Ala433
                                                     (1957) AGEGECERGIFGEAGGGGCTGGGGGTG
                                                     (2011) AGCCCCTGGTGCACGGCCTGCTGGCCCTG
                                 Consensus
Leu122-Ser199 Tryp427-Gly431
                                                     (2011) Avighteetheeverheineseraccentenseric
  Val127-Asn195-Arg426-Gly431
                                                     (2041)
                                                                ATCTGGGACGAGGCTGTGGGGTG
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Val120-Thr202-Ile424-Ala433

Leu122-Ser199-Arg426-Lys432	(2011)	ATCTGGGACGACCTGCGCAGCCTGTGCCTG
Leu122-Ser199-Arg426-Gly431	(2011)	ATCTGGGACGACCTGCGCAGCCTGTGCCTG
Lys121-Val200-Asn425-Lys432	(1999)	ATCTGGGAGGACCTGCGCAGCCTGTGCCTG
Val120-Ile201-Ile424-Ala433	(1987)	ATCTGGGACGACCTGCGCAGCCTGTGCCTG
Val120-Ile201B-Ile424-Ala433	(1987)	ATCTGGGAGGACCTGCGCAGCCTGTGCCTG
Consensus	(2041)	ATCTGGGACGACCTGCGCAGCCTGTGCCTG
		2071 2100
Leu122-Ser199 Tryp427-Gly431	(2041)	TTCAGGTACCACCGCCTGCGCGACCTGATC
Val127-Asn195-Arg426-Gly431	(2071)	TTCAGCTAGCACCGCCTGCGGGACCTGATC
Val120-Thr202-Ile424-Ala433	(2017)	TTEAGCTACCACCGCCTGCGCGACCTGATC
Leu122-Ser199-Arg426-Lys432	(2041)	TTCAGCTAGGACGGCCTGCGGGCCTGATC
Leu122-Ser199-Arg426-Gly431	(2041)	TTCAGCTACCACCGCCTGCGCGACCTGATC
Lys121-Val200-Asn425-Lys432	(2029)	TTCAGCTAGCACCGCCTGCGGGGCCTGATC
Val120-Ile201-Ile424-Ala433	(2017)	TTCAGCTACCACCGCCTGCGCGACCTGATC
Val120-Ile201B-Ile424-Ala433	(2017)	TTCAGETACCACCGCCTGCGCGACCTGATC
Consensus	(2071)	TTCAGCTACCACCGCCTGCGCGACCTGATC
0000.0	(20.2)	2101 2130
Leu122-Ser199 Tryp427-Gly431	(2071)	CTGATEGCEGEGEGEATEGTGCAGCTGCTG
Val127-Asn195-Arg426-Gly431	(2101)	CTGATEGEEGECEGEATEGTEGAGETGETG
Val120-Thr202-Ile424-Ala433	(2047)	CTGATCGCCGCCCGCATCGTGGAGCTGCTG
Leu122-Ser199-Arg426-Lys432	(2071)	CTGATCGCGCCCGCATCGTGGAGCTGCTG
Leu122-Ser199-Arg426-Gly431	(2071)	CTGATCGCCGCCGCATCGTGGAGCTGCTG
Lys121-Val200-Asn425-Lys432	(2059)	CTGATCGCCCCCGCATCGTGGAGCTGCTG
<del>-</del>		CTGATCGCCGCCGCATCGTGGAGCTGCTG
Val120-Ile201-Ile424-Ala433	(2047)	
Val120-Ile201B-Ile424-Ala433	(2047)	CTGATCGCGGCCCCCATCGTGGAGCTGCTG
Consensus	(2101)	CTGATCGCCGCCCGCATCGTGGAGCTGCTG
. 100 c 100 m	(0101)	2131 2160
Leu122-Ser199 Tryp427-Gly431	(2101)	ggeogdggggtgggaggcctgaagt <b>a</b> c
Val127-Asn195-Arg426-Gly431	(2131)	GGCGGCGCGCTGGGAGGCCCTGAAGTAC
Val120-Thr202-Ile424-Ala433	(2077)	GGCCGCGCGCTGGGAGGCCCTGAAGTAC
Leu122-Ser199-Arg426-Lys432	(2101)	GGCCGCCGCGGCTGGGAGGCCCTGAAGTAC
Leu122-Ser199-Arg426-Gly431	(2101)	GEGGGGGGGGGGGGGGGGGGGGAAGVAC
Lys121-Val200-Asn425-Lys432	(2089)	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Val120-Ile201-Ile424-Ala433	(2077)	EGGEGGGGGGGGGGGGGGGGGAGTAC
Val120-Ile201B-Ile424-Ala433	(2077)	EGECGECGEGETEGGAGGEGTGAAGTAC
Consensus	(2131)	GGCCGCCGCGGCTGGAGGCCCTGAAGTAC
		2161 2190
Leu122-Ser199 Tryp427-Gly431	(2131)	recees the rest covers of the second
Val127-Asn195-Arg426-Gly <b>43</b> 1	(2161)	TGGGGCAACCTGCTGCAGTACTGGATCCAG
Val120-Thr202-Ile424-Ala433	(2107)	TGGGGCAAGCEGGTGCAGTAGTGGATCCAG
Leu122-Ser199-Arg426-Lys <b>432</b>	(2131)	TEGGGEAATETEETEGAGTALTEGATCCAG
Leu122-Ser199-Arg426-Gly <b>43</b> 1	(2131)	TEGGERAACETECTEGAGRAUTEGATECAG
Lys121-Val200-Asn425-Lys <b>432</b>	(2119)	TGGGGCAAGETECTGGAGTACTGGATGCAG
Val120-Ile201-Ile424-Ala433	(2107)	EGGGGGAACC EGG TGCAGCACT GGATGCAG
Val120-Ile201B-Ile424-Ala433	(2107)	TEGEGRAACOTECTGCAG VACTEGATE CAG
Conse <b>nsus</b>	(2161)	TGGGGCAACCTGCTGCAGTACTGGATCCAG
	٠,	2191 2220
Leu122-Ser199 Tryp427-Gly431	(2161)	GAGGIGAAGAAGACGGCGTGAGCCHG1716
Val127-Asn195-Arg426-Gly431	(2191)	GAGCTGAAGAAWAGCGGEGTGAGGETGTTC
Val120-Thr202-Ile424-Ala433	(2137)	GAGCIGAAGAACAGCGCCGTGAGGCCTGTIC
Leu122-Ser199-Arg426-Lys432	(2161)	GAGCIGAAGAAGAGEGEGEGIGAGECTGILIC
Leu122-Ser199-Arg426-Gly431	(2161)	GAGCTGAAGAACAGEGCCGTGAGCCTGTTC
Lys121-Val200-Asn425-Lys432	(2149)	GAGCTGAAGAACAGCGGGGTGAGCCTGTTC
Val120-Ile201-Ile424-Ala433	(2137)	GAGCTGAAGAACAGCGCCGTGAGCCTGT <b>TC</b>
Val120-Ile201B-Ile424-Ala433	(2137)	GAGCTGAAGAACAGCGCCGTGAGECTGTTC
Consensus	(2191)	GAGCTGAAGAACAGCGCCGTGAGCCTGTTC
· ,	-	2221 2250
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Leu122-Ser199 Tryp427-Gly431
                               (2191) GACGCCATEGCCATCGCCGTGGCCGAGGGC
 Val127-Asn195-Arg426-Gly431
                               (2221) GACGCCATEGCCATEGCCGTGGCCGAGGGC
 Val120-Thr202-Ile424-Ala433
                               (2167) GACGCCATCGCCATCGCCGTGGCCGAGGGC
 Leu122-Ser199-Arg426-Lys432
                               (2191) GACGCCATCGCCATCGCCGTGGCCGAGGGC
                               (2191) GACGCCATCGCCATCGCCGTGGCCGAGGGC
 Leu122-Ser199-Arg426-Gly431
 Lys121-Val200-Asn425-Lys432
                               (2179)
                                      GACGCCATCGCCATCGCCGTGGCCGAGGGC
 Val120-Ile201-Ile424-Ala433
                               (2167)
                                      GACGCCATCGCCATCGCCGTGGCCGAGGGC
Val120-Ile201B-Ile424-Ala433
                               (2167) GACGCCATCGCCATCGCCGTGGCCGAGGGC
                    Consensus
                               (2221) GACGCCATCGCCATCGCCGTGGCCGAGGGC
                                      2251
Leu122-Ser199 Tryp427-Gly431
                               (2221) ACCGACCGCATCATCGAGGTGGCCCAGCGC
 Val127-Asn195-Arg426-Gly431
                               (2251) ACCGACCGCATCATCGAGGTGGCCCAGCGC
 Val120-Thr202-Ile424-Ala433
                               (2197) ACCGACCGCATCATCGAGGTGGCCCAGCGC
 Leu122-Ser199-Arq426-Lys432
                               (2221) ACCGACCGCATCATCGAGGTGGCCCAGCGC
 Leu122-Ser199-Arg426-Gly431
                               (2221) ACCGACCGCATCATCGAGGTGGCCCAGCGC
 Lys121-Val200-Asn425-Lys432
                               (2209) ACCGACCGCATCATCGAGGTGGCCCAGCGC
 Val120-Ile201-Ile424-Ala433
                               (2197) ACCGACCGCATCATCGAGGTGGCCCAGCGC
Val120-Ile201B-Ile424-Ala433
                               (2197) ACCGACCGCATCATCGAGGTGGCCCAGCGC
                   Consensus
                               (2251) ACCGACCGCATCATCGAGGTGGCCCAGCGC
Leu122-Ser199 Tryp427-Gly431
                               (2251) ATCGGCCGCGCCTTCCTGCACATCCCCCGC
 Val127-Asn195-Arq426-Gly431
                               (2281) ATCGGCCGCGCCTTCCTGCACATCCCCCGC
 Val120-Thr202-Ile424-Ala433
                               (2227) ATCGGCGCGCCCTTCCTGCACATCCCCCGC
 Leul22-Ser199-Arg426-Lys432
                               (2251) ATCGGCGCGCCCTTCCTGCACATCCCCCGC
 Leu122-Ser199-Arg426-Gly431
                                     ATCGGCCGCCTTCCTGCACATCCCCCGC
                               (2251)
                                     ATCGGCCGCGCCTTCCTGCACATCGCCCGC
 Lys121-Val200-Asn425-Lys432
                               (2239)
 Val120-Ile201-Ile424-Ala433
                               (2227)
                                     ATCGGCCGCGCCTTCCTGCACATCCCCCGC
Val120-Ile201B-Ile424-Ala433
                               (2227)
                                     (2281) ATCGGCCGCGCCTTCCTGCACATCCCCCGC
Leu122-Ser199 Tryp427-Gly431
                               (2281) CGCATCCCCCAGGGCTTCGAGGGGGGCCCTG
 Val127-Asn195-Arg426-Gly431
                               (2311) CGCATCCGCCAGGGGTTCGAGCGGGGGGGTG
                               (2257) EGCANCEGECAGEGETTEGAGEGEGECETE
 Val120-Thr202-Ile424-Ala433
 Leu122-Ser199-Arg426-Lys432
                               (2281) EGENTE EGEGGGGTTEGAGGGGGCCCCT
                               (2281) GCATCCGCCAGGGCTTCGAGCGGGCG
 Leu122-Ser199-Arg426-Gly431
 Lys121-Va1200-Asn425-Lys432
                               (2269) EGCATECESCAGESCUTEGAGESESCO
 Val120-Ile201-Ile424-Ala433
                               (2257)
                                     GCATCOGCCAGGCCTTCCCAGCCCGCCCTC
Val120-Ile201B-Ile424-Ala433
                              (2257) EGCATCCGCCAGGGCTTCGAGGGCGCCCCTG
                   Consensus
                               (2311)
                                     CGCATCCGCCAGGGCTTCGAGCGCGCCCTG
                                     2341
                                             2352
Leu122-Ser199 Tryp427-Gly431
                              (2311) CTGTAAGTCGAS
 Val127-Asn195-Arg426-Gly431
                              (2341)
                                     ONE VALORIE CON
 Val120-Thr202-Ile424-Ala433
                             -(2287)
                                     CHETAVACTECAT
                              (2311) PERUAN CON
Leu122-Ser199-Arg426-Lys432
                              (2311) CENTAL COLOR
Leu122-Ser199-Arg426-Gly431
Lys121-Val200-Asn425-Lys432
                             (2299) CTGTAACTCGAG
 Val120-Ile201-Ile424-Ala433
                              (2287) CIGTAACTCGAC
Val120-Ile201B-Ile424-Ala433
                              (2287) CTGTAACTCGAG
                   Consensus
                              (2341) CTGTAACTCGAG
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#### SEQ ID NO:3 VAL120-ALA204

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGGCGCCGGCGCCTGCCCCAA GGTGAGCTTCGAGCCCATCCCATCCACTACTGCGCCCCGCCGGCTTCGCCATCCTGAAGTG CAACGACAAGAAGTTCAACGGCAGCGGCCCCTGCACCAACGTGAGCACCGTGCAGTGCACCC ACGGCATCCGCCCGTGGTGAGCACCCAGCTGCTGCAACGGCAGCCTGGCCGAGGAGGGC GTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGA GAGCGTGGAGATCAACTGCACCCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGCC CCGGCCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACA TCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTC GGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAG CTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAA CAACACCATCGGCCCCAACAACACCCAACGGCACCATCACCCTGCCCTGCCGCATCAAGCAGA TCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCATCCGCGGCCAGATC CGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGCAAGGAGATCAGCAA CACCACCGAGATCTTCCGCCCCGGCGCGCGCGACATGCGCGACAACTGGCGCAGCGAGCTGT ACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAAGGCCAAGCGCCGC GTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCGCCATGTTCCTGGGCTTCCTGGGCGCCC GCCGGCAGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAG CGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCCCAGCAGCACCTGCTGC AGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCGCTACCTG AAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGT GCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATCTGGAACAACATGACCTGGA TGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCTACACCCTGATCGAGGAGAGC CAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGT GGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCG GCCTGGTGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCT ACAGCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCCGGGCCCCGACCGCCCCGAGGGCA TCGAGGAGGAGGGCGAGCGCGACCGCACCGCAGCAGCCCCCTGGTGCACGGCCTGCTG GCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCCTGCGCGACCTG ATCCTGATCGCCGCCCGCATCGTGGAGCTGCTGGGCCCGCCGCGGCTGGGAGGCCCTGAAGTAC TGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTCGA CGCCATCGCCATCGCCGAGGCCGAGCGCACCGCATCATCGAGGTGGCCCAGCGCATCG GCCGCGCCTTCCTGCACATCCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAAC **TCGAG** 

## SEQ ID NO:4 VAL120-ILE201

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGGCGGCATCACCCAGGCCTG GAAGTGCAACGACAAGAAGTTCAACGGCAGCGCCCCTGCACCAACGTGAGCACCGTGCAGT GCACCCACGCCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAG GAGGGCGTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCT GAAGGAGAGCGTGGAGATCAACTGCACCCGCCCAACAACAACACCCCGCAAGAGCATCACCA TCGGCCCGGCCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACT GCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCC CAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGAT GCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCAC CTGGAACAACACCATCGGCCCCAACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCA AGCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCATCCGCGGC CAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGCGGCAAGGAGAT CAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCGCAGCG AGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAAGGCCAAG CGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCGCCATGTTCCTGGGCTTCCTG GCTGAGCGGCATCGTGCAGCAGCAGCAGCACCTGCTGCGCGCCCATCGAGGCCCAGCAGCACC TGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCGC TACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCAC CGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATCTGGAACAACATGA CCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCTACACCCTGATCGAG GAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCAGCAAGTGGGCCA GCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCATGATCG TGGGCGGCCTGGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCC AGGGCTACAGCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCGCGGCCCCGACCGCCCCG CCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCCTGCG CGACCTGATCCTGATCGCCGCCCGCATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGGCCCT GAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCC GCATCGGCCGCCTTCCTGCACATCCCCCGCCGCATCCGCCAGGGCTTCGAGCGCCCCTGC **TGTAACTCGAG** 

## SEQ ID NO:5 VAL120-ILE201B

TTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCA CCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGTGCACAACGTGTGGGCCACCC ACGCCTGCGTGCCCACCGACCCCCAGGAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACA TGTGGAAGAACAACATGGTGGAGCAGATGCACGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGC CCTGCGTGCCCGGCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGC CCCCGCCGGCTTCGCCATCCTGAAGTGCAACGACAAGAAGTTCAACGGCAGCGGCCCCTGCACCAACGT GAGCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCT GGCCGAGGAGGGCGTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCT GAAGGAGAGCGTGGAGATCAACTGCACCCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGCCC CGGCCGCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGC GAGAAGTGGAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGACCATC GTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCGGCGGCGAGTTC TTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCAACAACACCAAC GGCACCATCACCCTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATG TACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACG GCGGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGCGACATGCGCGACAACTGGC GCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAAGGCCAAGC GCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCGCCATGTTCCTGGGCTTCCTGGGCGCCGC CGGCAGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGT GCAGCAGCAGAACAACCTGCTGCGCGCCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGG CTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAG CCTGGACCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCT GATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGAACGAGCAGGAGCTGCTGGAGCTGG ACAAGTGGGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCAT GATCGTGGGCGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAG GGCTACAGCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCGCGGCCCCGACCGCCCCGAGGGCATCG AGGAGGAGGGCGAGCGCGACCGCAGCAGCAGCCCCTGGTGCACGGCCTGCTGGCCCTGATCT GGGACGACCTGCGCAGCCTGTTCAGCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCCG CATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGGCCCTGAAGTACTGGGGCAACCTGCTGCAGTACTG GATCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCATCGCCGTGGCCGAGGGCAC CGACCGCATCATCGAGGTGGCCCAGCGCATCGGCCGCGCCTTCCTGCACATCCCCCGCCGCATCCGCCAG GGCTTCGAGCGCCCCTGCTGTAACTCGAGCGTGCT

#### **SEO ID NO:6 LYS121-VAL200**

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGGCCCCCGTGATCACCCA GGCCTGCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCGCCGGCTTCGC CATCCTGAAGTGCAACGACAAGAAGTTCAACGGCAGCGCCCCTGCACCAACGTGAGCACCG TGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCAACGGCAGCCTGG CCGAGGAGGCGTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTG CAGCTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCAACAACAACAACACCCGCAAGAGCAT CACCATCGGCCCGGCCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGC CCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGC AGGCCCAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATC GTGATGCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAAC AGCACCTGGAACAACACCATCGGCCCCAACAACACCCAACGGCACCATCACCCTGCCCTGCCCG CATCAAGCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCATCC GCGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAG GAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCG CAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAAGG CCAAGCGCCGCGTGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCCCATGTTCCTGGGC TTCCTGGGCGCCGCCGCAGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGCAGGCCCGC CAGCTGCTGAGCGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCCAGCA GCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGG AGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGC ACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATCTGGAACAA CATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCTACACCCTGA TCGAGGAGACCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCAGGAGCTGGACAAGTG GGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCAT GATCGTGGGCGGCCTGGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGT GCGCCAGGGCTACAGCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCCGGGCCCCGACCG CCCCGAGGGCATCGAGGAGGAGGGCGCGAGCGCGACCGCAGCAGCCCCCTGGTGC ACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCC TGCGCGACCTGATCCTGATCGCCGCCCGCATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGG CCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTG CAGCGCATCGGCCGCCTTCCTGCACATCCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCC CTGCTGTAACTCGAGCGTGCT

## **SEQ ID NO:7: LEU122-SER199**

GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGGGCAACAGCGTGAT CACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGG CTTCGCCATCCTGAAGTGCAACGACAAGAAGTTCAACGGCAGCGGCCCCTGCACCAACGTGA GCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCAACGGC AGCCTGGCCGAGGAGGGCGTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCAT CATCGTGCAGCTGAAGGAGCGTGGAGATCAACTGCACCCGCCCCAACAACAACACCCGCA AGAGCATCACCATCGGCCCGGCCGCCCTTCTACGCCACCGGCGACATCATCGGCGACATCC GCCAGGCCCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACC AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGCGGCGACCC CGAGATCGTGATGCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCT GTTCAACAGCACCTGGAACAACACCATCGGCCCCAACAACACCCAACGGCACCATCACCCTGC CCTGCCGCATCAAGCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCC CCCATCCGCGGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGC GGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGCGCGACATGCGCGACAA CTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCA CCAAGGCCAAGCGCGCGTGGTGCAGCGCGAGAAGCGCGCGTGACCCTGGGCGCCATGTTC CTGGGCTTCCTGGGCGCCGCCGCAGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGCAG GCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGC CCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGG CCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTG ATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATCTG GAACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCTACA CCCTGATCGAGGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGA CAAGTGGGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTT CATCATGATCGTGGGCGGCCTGGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAA CCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCCGCGCCCC CTGGTGCACGGCCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTAC CACCGCCTGCGCGACCTGATCCTGATCGCCGCCCGCATCGTGGAGCTGCTGGGCCGCCGCGCGCC TGGGAGGCCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAG GGTGGCCCAGCGCATCGGCCGCGCCTTCCTGCACATCCCCCGCCGCATCCGCCAGGGCTTCGA GCGCGCCCTGCTGTAACTCGAGCGTGCT

#### SEQ ID NO:8 VAL120-THR202

GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGGGCGGCGCCACCCAGGCCTG GAAGTGCAACGACAAGAAGTTCAACGGCAGCGGCCCCTGCACCAACGTGAGCACCGTGCAGT GCACCCACGCATCCGCCCGTGGTGAGCACCCAGCTGCTGCTGAACGCCAGCCTGGCCGAG GAGGGCGTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCT GAAGGAGAGCGTGGAGATCAACTGCACCCGCCCAACAACAACACCCGCAAGAGCATCACCA TCGGCCCGGCCGCCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACT GCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCC CAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGAT GCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCAC CTGGAACAACACCATCGGCCCCAACAACACCCAACGGCACCATCACCCTGCCCTGCCGCATCA AGCAGATCATCAACCGCTGGCAGGAGGTGGGCAAGGCCATGTACGCCCCCCCATCCGCGGC CAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGCAAGGAGAT CAGCAACACCACCGAGATCTTCCGCCCCGGCGCGCGCGACACTGCGCGACAACTGGCGCAGCG AGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCACCAAGGCCAAG CGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCGCCATGTTCCTGGGCTTCCTG GCTGAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCCCATCGAGGCCCAGCAGCACC TGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCGC TACCTGAAGGACCAGCAGCTGCTGGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCAC CGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATCTGGAACAACATGA CCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCTACACCCTGATCGAG GAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCA GCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCATGATCG TGGGCGCCTGGTGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCC AGGGCTACAGCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCGCGGCCCCGACCGCCCCG AGGGCATCGAGGAGGAGGGCGCGAGCGCGACCGCAGCAGCCCCCTGGTGCACGG CCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCCTGCG CGACCTGATCCTGATCGCCGCCCGCATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGGCCCT GAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCC TGTTCGACGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCCCAGC GCATCGCCGCCCCTTCCTGCACATCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGC **TGTAACTCGAG** 

#### **SEQ ID NO:9 TRP427-GLY431**

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCCAAGAGCAGCAACTGGAAGGAGAT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAGC TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCGCCGGCTTCGCCATCCTGAAGTGCAACGACAAGAA GTTCAACGCAGCGCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC CCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGC AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGCCCCGGCCGCCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAG AAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGCGCGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCATCG GGGGCGCAAGGCCATGTACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACATC ACCGGCCTGCTGACCCGCGACGGCGCAAGGAGATCAGCAACACCACCGAGATCTTCCG CCCCGGCGGCGCGACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGTGGTGA AGATCGAGCCCCTGGGCGTGGCCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAAG CGCGCCGTGACCCTGGGCGCCATGTTCCTGGGCTTCCTGGGCGCCGCCGGCAGCACCATGGGC GCCGCAGCCTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCA GAACAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCA TCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTG GGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTG ATCGACAACTACACCAACCTGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGAA GAACGAGCAGGAGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTCGACATCA GCAAGTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTGGTGGGCCTGCGCA TCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCC AGACCGCTTCCCGCCCCCGCGGCCCGACCGCCCGAGGGCATCGAGGAGGGGGGGCGGC GAGCGCGACCGCACCAGCAGCCCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACGA CCTGCGCAGCCTGTTCAGCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCCG CATCGTGGAGCTGCTGGCCGCCGCGGCTGGGAGGCCCTGAAGTACTGGGGCAACCTGCTGC AGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCATCGCC GTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCCCAGCGCATCGGCCGCCTTCCTGCA CATCCCCGCCGCATCCGCCAGGGCTTCGAGCGCCCCTGCTGTAACTCGAG

#### **SEQ ID NO:10 ARG426-GLY431**

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGAACT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAGC TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCGCCGGCTTCGCCATCCTGAAGTGCAACGACAAGAA GTTCAACGCAGCGCCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC CCGTGGTGAGCACCCAGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGC AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGCCCCGGCCGCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAG AAGTGGAACAACACCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGGGGGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCATCG GCCCAACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAAGCAGATCATCAACCGC GGCGGCGCAAGGCCATGTACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACAT CACCGGCCTGCTGCTGACCCGCGACGGCGCAAGGAGATCAGCAACACCACCGAGATCTTCC GCCCGGCGCGCGACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTG AAGATCGAGCCCTGGGCGTGGCCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAA GCGCGCCGTGACCCTGGGCGCCATGTTCCTGGGCTTCCTGGGCGCCGCCGCCAGCACCATGGG CGCCGCAGCCTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGC AGAACAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGC ATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCCTACCTGAAGGACCAGCAGCTGCT GGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCT GATCGACAACTACACCAACCTGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGA AGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTCGACATC AGCAAGTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTGGTGGGCCTGCGC ATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTC CAGACCGCTTCCCGCCCCCGCGGCCCCGACGCCCCGAGGGCATCGAGGAGGAGGGCGG CGAGCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACG ACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCC GCATCGTGGAGCTGCTGGGCCGCCGCGCTGGGAGGCCCTGAAGTACTGGGGCAACCTGCTG CAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCATCGC CGTGGCCGAGGGCACCGACCGCATCATCGAGGTGGCCCAGCGCATCGGCCGCGCCTTCCTGC ACATCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAACTCGAG

#### SEQ ID NO:11 ARG426-GLY431B

GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGCAGCAACTGGAAGGGAGAT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAGC TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCGCCGGCTTCGCCATCCTGAAGTGCAACGACAAGAA GTTCAACGGCAGCGCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC CCGTGGTGAGCACCCAGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGC AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGCCCCGGCCGCCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAG AAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCATCG GCCCAACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAAGCAGATCATCAACCGC GGCAGCGGCAAGGCCATGTACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACAT CACCGGCCTGCTGACCCGCGACGGCGCAAGGAGATCAGCAACACCACCGAGATCTTCC GCCCGGCGGCGCGACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGTGGTG AAGATCGAGCCCTGGGCGTGGCCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAA GCGCGCCGTGACCCTGGGCGCCATGTTCCTGGGCTTCCTGGGCGCCGCCGCCAGCACCATGGG CGCCGCAGCCTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGC AGAACAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGC ATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCT GGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCT GATCGACAACTACACCAACCTGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGA AGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTCGACA**TC** ATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTC CAGACCCGCTTCCCCGCCCCCGCGGCCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGG CGAGCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACG ACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCC GCATCGTGGAGCTGCTGGGCCGCCGCGCGGGTGGGAGGCCCTGAAGTACTGGGGCAACCTGCTG CAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCATCGC CGTGGCCGAGGGCACCGCATCATCGAGGTGGCCCAGCGCATCGGCCGCCTTCCTGC ACATCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAACTCGAG

#### **SEQ ID NO:12 ARG426-LYS432**

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGAT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAGC TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCGCCGGCTTCGCCATCCTGAAGTGCAACGACAAGAA GTTCAACGCAGCGCCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC CCGTGGTGAGCACCCAGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGC AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGCCCCGGCCGCCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAG AAGTGGAACAACACCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCCATCG GCCCAACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAAGCAGATCATCAACCGC GGCGGCAACAAGGCCATGTACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACAT CACCGCCTGCTGCCCGCCGCGCGCGCGCAGGATCAGCAACACCACCGAGATCTTCC GCCCGGCGGCGACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTG AAGATCGAGCCCTGGGCGTGGCCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAA GCGCGCGTGACCCTGGGCGCATGTTCCTGGGCTTCCTGGGCGCCGCCGCAGCACCATGGG CGCCGCAGCCTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGCATCGTGCAGCAGC AGAACAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGC ATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCT GGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCT GATCGACAACTACACCAACCTGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGA AGAACGAGCAGGAGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTCGACATC AGCAAGTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCCGCCTGGTGGGCCTGCGC ATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTC CAGACCCGCTTCCCCGCCCCCCGCGCCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGG CGAGCGCGACCGCAGCAGCCCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACG ACCTGCGCAGCCTGTTCCGCTACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCC GCATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGGCCCTGAAGTACTGGGGCAACCTGCTG CAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCATCGC CGTGGCCGAGGGCACCGCATCATCGAGGTGGCCCAGCGCATCGGCCGCCTTCCTGC ACATCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAACTCGAG

#### **SEQ ID NO:13 ASN425-LYS432**

GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGCAACTGGAAGGAGAT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAGC TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCGCCGGCTTCGCCATCCTGAAGTGCAACGACAAGAA GTTCAACGGCAGCGCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC CCGTGGTGAGCACCCAGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGC AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCGCCCAACAACACCCGCAAGAGCATCACCATCGGCCCGGCCGCCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAG AAGTGGAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCATCG GCCCAACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAAGCAGATCATCAACGCCC CCAAGGCCATGTACGCCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACATCACCGGCC TGCTGCTGACCCGCGACGGCGGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGC GGCGGCGACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGA GCCCTGGGCGTGGCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCG TGACCCTGGGCGCCATGTTCCTGGGCTTCCTGGGCGCCGCCGCAGCACCATGGGCGCCCGCA GCCTGACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGCAGCAACAAC CTGCTGCGCGCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCA GCTGCAGGCCGCGTGCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCT GGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAAC CTACACCAACCTGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGC AGGAGCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGG CTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTGGTGGGCCTGCGCATCGTGTTC ACCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCCAGACCCGC TTCCCCGCCCCCGCGCCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGCGAGCGCGA CCGCGACCGCAGCAGCCCCTGGTGCACGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAG GCTGCTGGGCCGCCGCGGTGGGAGGCCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGA TCCAGGAGCTGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCATCGCCGTGGCCGAG GGCACCGACCGCATCATCGAGGTGGCCCAGCGCATCGGCCGCGCTTCCTGCACATCCCCCGC CGCATCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAACTCGAG

#### **SEQ ID NO:14 ILE424-ALA433**

GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGAT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAGC TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCGCCGCCGCCTTCGCCATCCTGAAGTGCAACGACAAGAA GTTCAACGCCACCGCCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC  ${\tt CCGTGGTGAGCACCCAGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGC}$ AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGCCCCGGCCGCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAG AAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCCATCG GCCCAACAACACCAACGGCACCATCACCCTGCCCTGCCGCATCAAGCAGATCATCGGCGGC GCCATGTACGCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTG CTGACCGCGACGGCGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGCGCGG CGACATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCC TGGGCGTGGCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACC CTGGGCGCCATGTTCCTGGGCTTCCTGGGCGCCGCCGCAGCACCATGGGCGCCCGCAGCCTG ACCCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGCAGCAACCACCTGCT  ${\tt GCGCGCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGC}$ AGGCCGCGTGCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGC TGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAG CCTGGACCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACA CCAACCTGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGA GCTGCTGGAGCTGGACAAGTGGGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGT GGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTGGTGGGCCTGCGCATCGTGTTCACCG TGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCC CCGCCCCCGCGGCCCCGACCGCCCCGAGGGCATCGAGGAGGAGGGCGGCGAGCGCGACCGC GACCGCAGCAGCCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTG CTGGGCCGCCGCGGCTGGGAGGCCCTGAAGTACTGGGCCAACCTGCTGCAGTACTGGATCCA GGAGCTGAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCATCGCCGTGGCCGAGGGCA CCGACCGCATCATCGAGGTGGCCCAGCGCATCGGCCGCCGCCTTCCTGCACATCCCCCGCCGCA TCCGCCAGGGCTTCGAGCGCGCCCTGCTGTAACTCGAG

## **SEQ ID NO:15 ILE423-MET434**

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGAT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCA**G**C TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCCGCCGGCTTCGCCATCCTGAAGTGCAACGACAAGAA GTTCAACGGCAGCGGCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC CCGTGGTGAGCACCCAGCTGCTGAACGGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGC AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCCGCCCAACAACAACACCCGCAAGAGCATCACCATCGGCCCCGGCCGCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAG AAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCATCG TACGCCCCCCATCCGCGGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACC CGCGACGGCGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGCGACAT GCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCG TGGCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGC GCCATGTTCCTGGGCTTCCTGGGCGCCGCCGCAGCACCATGGGCGCCCGCAGCCTGACCCTG ACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGCAGCACCAGCTGCTGCGCGC CATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCC GCGTGCTGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGC GGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGA CCAGATCTGGAACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACC TGATCTACACCCTGATCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTG GAGCTGGACAAGTGGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACAT CAAGATCTTCATCATGATCGTGGGCGGCCTGGTGGGCCTGCGCATCGTGTTCACCGTGCTGAG CATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCC CCGCGGCCCGACCGCCCGAGGGCATCGAGGAGGAGGGCGCGAGCGGACCGCGACCGC AGCAGCCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTG CGCCGCGGCTGGGAGCCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCT GAAGAACAGCGCCGTGAGCCTGTTCGACGCCATCGCCATCGCCGTGGCCGAGGGCACCGACC GCATCATCGAGGTGGCCCAGCGCATCGGCCGCCCTTCCTGCACATCCCCCGCCGCATCCGCC AGGGCTTCGAGCGCCCCTGCTGTAACTCGAG

#### **SEQ ID NO:16 GLN422-TYR435**

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGAT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAGC TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCGCCGCTTCGCCATCCTGAAGTGCAACGACAAGAA GTTCAACGCAGCGCCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC CCGTGGTGAGCACCCAGCTGCTGAACGCAGCCTGGCCGAGGAGGGCGTGGTGATCCGC AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCGCCCAACAACACCCGCAAGAGCATCACCATCGGCCCGGCCGCCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCGAG AAGTGGAACAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCATCG CCCCCATCCGCGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGACCCGCGAC GGCGGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGA CAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCC CCACCAAGGCCAAGCGCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCGCCATG TTCCTGGGCTTCCTGGGCGCCGCCGGCAGCACCATGGGCGCCCGCAGCCTGACCGTG CAGGCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGCACAACCTGCTGCGCGCCATCGA GGCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGC TGGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAG CTGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGAT CTGGAACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCT ACACCTGATCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCT GGACAAGTGGGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGA TCTTCATCATGATCGTGGGCGGCCTGGTGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCG TGAACCGCGTGCGCCAGGGCTACAGCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCGCG GCCCGACCGCCCGAGGGCATCGAGGAGGAGGGCGCGAGCGCGACCGCACCGCAGCAG CCCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAG CGGCTGGGAGGCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGA ATCGAGGTGGCCAGCGCATCGGCCGCGCTTCCTGCACATCCCCCGCCGCATCCGCCAGGGC TTCGAGCGCGCCCTGCTGTAACTCGAG

#### SEQ ID NO:17 GLN422-TYR435B

GAATTCGCCACCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCA GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTG ACCCTGCACTGCACCAACCTGAAGAACGCCACCAACACCAAGAGCAGCAACTGGAAGGAGAT GGACCGCGGCGAGATCAAGAACTGCAGCTTCAAGGTGACCACCAGCATCCGCAACAAGATGC AGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCATCGACAACGACAACACCAGC TACAAGCTGATCAACTGCAACACCAGCGTGATCACCCAGGCCTGCCCCAAGGTGAGCTTCGA GCCCATCCCATCCACTACTGCGCCCCGCCGCCGCCTCCCATCCTGAAGTGCAACGACAAGAA GTTCAACGGCAGCGGCCCTGCACCAACGTGAGCACCGTGCAGTGCACCCACGGCATCCGCC CCGTGGTGAGCACCCAGCTGCTGAACGGCAGCCTGGCCGAGGAGGCCGTGGTGATCCGC AGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGAT CAACTGCACCGCCCCAACAACACACCCGCAAGAGCATCACCATCGGCCCGGCCGCCCT TCTACGCCACCGGCGACATCATCGGCGACATCCGCCAGGCCCACTGCAACATCAGCGGCG**AG** AAGTGGAACACCCTGAAGCAGATCGTGACCAAGCTGCAGGCCCAGTTCGGCAACAAGAC CATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCCGAGATCGTGATGCACAGCTTCAACTGCG GCGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACAGCACCTGGAACAACACCATCG GCCCAACAACACCAACGCACCATCACCCTGCCCTGCCGCATCAAGCAGGCCCCCTACGCCC CCCCATCCGCGCCAGATCCGCTGCAGCAGCACATCACCGGCCTGCTGCTGACCCGCGACG GCGGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGAC AACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCC CACCAAGGCCAAGCGCGCGTGGTGCAGCGCGAGAAGCGCGCGTGACCCTGGGCGCCATGT TCCTGGGCTTCCTGGGCGCCGCCGGCAGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGC AGGCCGCCAGCTGCTGAGCGCCATCGTGCAGCAGCAGCACCACCTGCTGCGCGCCATCGAG GCCCAGCAGCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCT GGCCGTGGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGC TGATCTGCACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATC TGGAACAACATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCTA CACCTGATCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTG GACAAGTGGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGAT CTTCATCATGATCGTGGCGGCCTGGTGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGT GAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCCGCGG CCCCGACCGCCCGAGGGCATCGAGGAGGAGGGCGCGAGCGCGACCGCAGCAGCAGC CCCTGGTGCACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGC TACCACCGCCTGCGCGACCTGATCCTGATCGCCGCCCGCATCGTGGAGCTGCTGGGCCGCCGC GGCTGGAGCCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAA CGAGGTGGCCAGCGCATCGGCCGCCTTCCTGCACATCCCCCGCCATCCGCCAGGGCTT CGAGCGCCCTGCTGTAACTCGAG

#### SEO ID NO:18: LEU122-SER199; ARG426-GLY431

GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGGGCAACAGCGTGAT CACCCAGGCCTGCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCGCCGG CTTCGCCATCCTGAAGTGCAACGACAAGAAGTTCAACGGCAGCGGCCCCTGCACCAACGTGA GCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCAACGGC AGCCTGGCCGAGGAGGGCGTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCAT CATCGTGCAGCTGAAGGAGCGTGGAGATCAACTGCACCCGCCCCAACAACAACACCCGCA AGAGCATCACCATCGGCCCGGCCGCCCTTCTACGCCACCGGCGACATCATCGGCGACATCC GCCAGGCCCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACC AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGCGGCGACCC CGAGATCGTGATGCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCT GTTCAACAGCACCTGGAACAACACCATCGGCCCCAACAACACCCAACGGCACCATCACCCTGC CCTGCCGCATCAAGCAGATCATCAACCGCGGCGGCGGCAAGGCCATGTACGCCCCCCCATCC GCGGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAG GAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCG CAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAAGG CCAAGCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCGCCATGTTCCTGGGC TTCCTGGGCGCCGCCGCAGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGCAGGCCCGC CAGCTGCTGAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCCAGCA GCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGG AGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGC ACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATCTGGAACAA CATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCTACACCCTGA TCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTG GGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCAT GATCGTGGGCGCCTGGTGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGT GCGCCAGGGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCCGCGCCCCGACCG CCCCGAGGCATCGAGGAGGAGGGCGCGAGCGCGACCGCAGCAGCCCCCTGGTGC ACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCC TGCGCGACCTGATCCTGATCGCCGCCCGCATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGG CCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTG CAGCGCATCGGCCGCCTTCCTGCACATCCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCC CTGCTGTAACTCGAG

## SEQ ID NO:19 LEU122-SER199; ARG426-LYS432

GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGGGCAACAGCGTGAT CACCCAGGCCTGCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCGCCGG CTTCGCCATCCTGAAGTGCAACGACAAGAAGTTCAACGGCAGCGGCCCCTGCACCAACGTGA GCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC AGCCTGGCCGAGGGGGGGTGGTGATCCGCAGCGAGACTTCACCGACAACGCCAAGACCAT CATCGTGCAGCTGAAGGAGCGTGGAGATCAACTGCACCCGCCCAACAACAACACCCGCA AGAGCATCACCATCGGCCCGGCCGCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCC GCCAGGCCCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACC AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGCGGCGACCC CGAGATCGTGATGCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCT GTTCAACAGCACCTGGAACAACACCATCGGCCCCAACAACACCAACGGCACCATCACCCTGC GCGGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAG GAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCG CAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAAGG TTCCTGGGCGCCGCGGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGCAGGCCCGC CAGCTGCTGAGCGCATCGTGCAGCAGCAGCACCACCTGCTGCGCGCCATCGAGGCCCAGCA GCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGG AGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGC ACCACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATCTGGAACAA CATGACCTGGATGGAGGGGGGGGGGGAGATCGACAACTACACCAACCTGATCTACACCCTGA TCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTG GGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCAT GATCGTGGCGGCCTGGTGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGT GCGCCAGGGCTACAGCCCCCTGAGCTTCCAGACCCGCTTCCCCGCCCCCCGCGCCCCGACCG CCCCGAGGCATCGAGGAGGAGGGCGCGAGCGCGACCGCAGCAGCCCCCTGGTGC ACGCCTGCTGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCC TGCGCGACCTGATCCTGATCGCCGCCGCATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGG CCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTG CAGCGCATCGGCCGCCTTCCTGCACATCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCC **CTGCTGTAACTCGAG** 

#### SEQ ID NO: 20: LEU122-SER199; TRP427-GLY431

GTCTTCGTTTCGCCCAGCGCCGTGGAGAAGCTGTGGGTGACCGTGTACTACGGCGTGCCCGTG TGGAAGGAGGCCACCACCACCTGTTCTGCGCCAGCGACGCCAAGGCCTACGACACCGAGGT GCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAACCCCCAGGAGATCGTGCT GGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTGGAGCAGATGCACGAG GACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCTGCGTGAAGCTGGGCAACAGCGTGAT CACCCAGGCCTGCCCCAAGGTGAGCTTCGAGCCCATCCCATCCACTACTGCGCCCCGCCGG CTTCGCCATCCTGAAGTGCAACGACAAGAAGTTCAACGGCAGCGGCCCCTGCACCAACGTGA GCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGC AGCCTGGCCGAGGAGGCGTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCAT CATCGTGCAGCTGAAGGAGCGTGGAGATCAACTGCACCCGCCCAACAACAACACCCGCA AGAGCATCACCATCGGCCCGGCCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCC GCCAGGCCCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACC AAGCTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGGCGGCGACCC CGAGATCGTGATGCACAGCTTCAACTGCGGCGGCGAGTTCTTCTACTGCAACAGCACCCAGCT GTTCAACAGCACCTGGAACAACACCATCGGCCCCAACAACACCCAACGGCACCATCACCCTGC GCGCCAGATCCGCTGCAGCAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAG GAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCG CAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTGGGCGTGGCCCCCACCAAGG CCAAGCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACCCTGGGCCCATGTTCCTGGGC TTCCTGGGCGCCGGCAGCACCATGGGCGCCCGCAGCCTGACCCTGACCGTGCAGGCCCGC CAGCTGCTGAGCGCATCGTGCAGCAGCAGCAACCTGCTGCGCGCCATCGAGGCCCAGCA GCACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGG AGCGCTACCTGAAGGACCAGCAGCTGCTGGGCCATCTGGGGCTGCAGCGGCAAGCTGATCTGC ACCACCGCCGTGCCTGGAACGCCAGCTGGAGCAACAAGAGCCTGGACCAGATCTGGAACAA CATGACCTGGATGGAGTGGGAGCGCGAGATCGACAACTACACCAACCTGATCTACACCCTGA TCGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTG GGCCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCAT GATCGTGGGCGGCCTGGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACCGCGT GCGCCAGGGCTACAGCCCCTGAGCTTCCAGACCGGCTTCCCCGCCCCCCGGGGCCCGACCG CCCCGAGGCCATCGAGGAGGAGGGCGCGAGCGCGACCGCAGCAGCCCCCTGGTGC ACGGCCTGCTGGCCCTGATCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTACCACCGCC ·TGCGCGACCTGATCCTGATCGCCGCCCGCATCGTGGAGCTGCTGGGCCGCCGCGGCTGGGAGG CCCTGAAGTACTGGGGCAACCTGCTGCAGTACTGGATCCAGGAGCTGAAGAACAGCGCCGTG CAGCGCATCGGCCGCCTTCCTGCACATCCCCCGCCGCATCCGCCAGGGCTTCGAGCGCGCC **CTGCTGTAACTCGAG** 

# SEQ ID NO:21 LYS121-VAL200; ASN425-LYS432

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## SEQ ID NO:22 VAL120-ILE201; ILE 424-ALA433

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#### SEQUENCE LISTING

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- Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His 705 710 715 720
- Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu 725 730 735
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- Leu Leu Asn Gly Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser
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- Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu 275 280 285
- Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser 290 295 300
- Ile Thr Ile Gly Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile 305 310 315 320
- Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn 325 330 335
- Asn Thr Leu Lys Gln Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn 340 345 350
- Lys Thr Ile Val Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val 355 360 365
- Met His Ser Phe Asn Cys Gly Glu Phe Phe Tyr Cys Asn Ser Thr 370 375 380
- Gln Leu Phe Asn Ser Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr 385 390 395 400
- Asn Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg 405 410 415
- Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln 420 425 430
- Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
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- Gly Lys Glu Ile Ser Asn Thr Thr Glu Ile Phe Arg Pro Gly Gly Gly 450 455 460
- Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val 465 470 475 480
- Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val
  485 490 495
- Val Gln Arg Glu Lys Arg Ala Val Thr Leu Gly Ala Met Phe Leu Gly 500 505 510
- Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Leu Thr Leu 515 520 525
- Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn 530 535 540
- Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr 545 550 555 560

Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg 565 570 575

- Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys
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- Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys
  595 600 605
- Ser Leu Asp Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Glu Arg 610 615 620
- Glu Ile Asp Asn Tyr Thr Asn Leu Ile Tyr Thr Leu Ile Glu Glu Ser 625 630 635 640
- Gln Asn Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys 645 650 655
- Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile Ser Lys Trp Leu Trp Tyr 660 665 670
- Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile 675 680 685
- Val Phe Thr Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser 690 695 700
- Pro Leu Ser Phe Gln Thr Arg Phe Pro Ala Pro Arg Gly Pro Asp Arg 705 710 715 720
- Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser
  725 730 735
- Ser Pro Leu Val His Gly Leu Leu Ala Leu Ile Trp Asp Asp Leu Arg
  740 745 750
- Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Ile Leu Ile 755 760 765
- Ala Ala Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu 770 775 780
- Lys Tyr Trp Gly Asn Leu Leu Gln Tyr Trp Ile Gln Glu Leu Lys Asn 785 790 795 800
- Ser Ala Val Ser Leu Phe Asp Ala Ile Ala Ile Ala Val Ala Glu Gly 805 810 815
- Thr Asp Arg Ile Ile Glu Val Ala Gln Arg Ile Gly Arg Ala Phe Leu 820 825 830
- His Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Arg Ala Leu Leu 835 840 845

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<211> 2310

<212> DNA

<213> Artificial Sequence

PCT/US99/31272 WO 00/39303

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ctgaacggca gcctggccga ggagggcgtg gtgatccgca gcgagaactt caccgacaac 600
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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
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gccggcttcg ccatcctgaa gtgcaacgac aagaagttca acggcagcgg cccctgcacc 480
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ctgaacggca gcctggccga ggagggcgtg gtgatccgca gcgagaactt caccgacaac 600
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ctgaagcaga tcgtgaccaa gctgcaggcc cagttcggca acaagaccat cgtgttcaag 840
cagagcageg geggegaece egagategtg atgeacaget teaactgegg eggegagtte 900
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<212> DNA
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Lys121-Val200

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<223> Description of Artificial Sequence: Vall20-Thr202
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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
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gccacccagg cctgccccaa ggtgagcttc gagcccatcc ccatccacta ctgcgccccc 420
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gccaagacca tcatcgtgca gctgaaggag agcgtggaga tcaactgcac ccgccccaac 660
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<212> DNA
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence: Trp427-Gly431

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<223> Description of Artificial Sequence: Arg426-Gly431
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cagatgcacg aggacatcat cagcetgtgg gaccagagee tgaageectg egtgaagetg 360
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<210> 11
<211> 2541
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Arg426-Gly431B
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agcatcegca acaagatgca gaaggagtac geeetgttet acaagetgga egtggtgeee 540

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<211> 2541
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<223> Description of Artificial Sequence: Arg426-Lys432
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<210> 13
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<223> Description of Artificial Sequence: Asn425-Lys432
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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
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ggcggcgacc ccgagatcgt gatgcacagc ttcaactgcg gcggcgagtt cttctactgc 1140
aacagcaccc agctgttcaa cagcacctgg aacaacacca tcggccccaa caacaccaac 1200
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ggegtggecc ccaccaagge caagegeege gtggtgeage gegagaageg egeegtgaee 1500
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ile424-Ala433

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
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gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
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agcatccgca acaagatgca gaaggagtac gccctgttct acaagctgga cgtggtgccc 540
atcgacaacg acaacaccag ctacaagctg atcaactgca acaccagcgt gatcacccag 600
geetgeecca aggtgagett egageecate eccatecaet aetgegeece egeeggette 660
gccatcctga agtgcaacga caagaagttc aacggcagcg gcccctgcac caacgtgagc 720
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ile423-Met434

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<211> 2517
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Gln422-Tyr435
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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
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PCT/US99/31272 WO 00/39303

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<211> 2517
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Gln422-Tyr435B
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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
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accedentiate geogramment accedentation acced
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<211> 2322
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<213> Artificial Sequence

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<210> 19 <211> 2322 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu122-Ser199;
 Arg426-Lys432

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geagtetteg tttegeceag egeegtggag aagetgtggg tgaeegtgta etaeggegtg 120

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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccacccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcetgtgg gaccagagee tgaageeetg egtgaagetg 360
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tactgcgccc ccgccggctt cgccatcctg aagtgcaacg acaagaagtt caacggcagc 480
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gccaccggcg acatcatcgg cgacatccgc caggcccact gcaacatcag cggcgagaag 780
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tacaaggtgg tgaagatcga gcccctgggc gtggccccca ccaaggccaa gcgccgcgtg 1260
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ggccgccgcg gctgggaggc cctgaagtac tggggcaacc tgctgcagta ctggatccag 2160
gagetgaaga acagegeegt gageetgtte gaegeeateg ceategeegt ggeegaggge 2220
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<210> 20
<211> 2322
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Leu122-Ser199;
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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccacccac gcctgcgtgc ccaccgaccc caacccccag 240
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acccagctgc tgctgaacgg cagcctggcc gaggagggcg tggtgatccg cagcgagaac 600
ttcaccgaca acgccaagac catcatcgtg cagctgaagg agagcgtgga gatcaactgc 660
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ggccgccgcg gctgggaggc cctgaagtac tggggcaacc tgctgcagta ctggatccag 2160
gagetgaaga acagegeegt gageetgtte gaegeeateg ceategeegt ggeegaggge 2220
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<210> 21
<211> 2310
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Lys121-Val200;
      Asn425-Lys432
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gcagtcttcg tttcgcccag cgccgtggag aagctgtggg tgaccgtgta ctacggcgtg 120
cccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgccaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccacccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
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cccgtgatca cccaggcctg ccccaaggtg agcttcgagc ccatccccat ccactactgc 420
geocegeeg gettegeeat cetgaagtge aacgacaaga agtteaacgg cageggeece 480
tgcaccaacg tgagcaccgt gcagtgcacc cacggcatcc gccccgtggt gagcacccag 540
ctgctgctga acggcagcct ggccgaggag ggcgtggtga tccgcagcga gaacttcacc 600
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<210> 22
<211> 2298
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<223> Description of Artificial Sequence: Val120-Ile201;
      Ile424-Ala433
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cccgtgtgga aggaggccac caccaccctg ttctgcgcca gcgacgccaa ggcctacgac 180
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PCT/US99/31272 WO 00/39303

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<210> 23
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<211> 2298 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val120-Ile201B; Ile424-Ala433

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cccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgccaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccacccac gcctgcgtgc ccaccgaccc caacccccag 240
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aacaacaccc gcaagagcat caccategge eceggeegeg cettetaege caceggegae 720
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aagtactggg gcaacctgct gcagtactgg atccaggagc tgaagaacag cgccgtgagc 2160
ctgttcgacg ccatcgccat cgccgtggcc gagggcaccg accgcatcat cgaggtggcc 2220
cagegeateg geogegeett cetgeacate eccegeogea teegecaggg ettegagege 2280
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2298

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cccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgccaa ggcctacgac 180
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<212> DNA

<213> Artificial Sequence

<220>

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cccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgccaa ggcctacgac 180
accgaggtgc acaacgtgtg ggccacccac gcctgcgtgc ccaccgaccc caacccccag 240
gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
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aaggtgaget tegageeeat ecceateeac tactgegeec cegeeggett egeeateetg 480
aagtgcaacg acaagaagtt caacggcagc ggcccctgca ccaacgtgag caccgtgcag 540
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gaggagggcg tggtgatccg cagcgagaac ttcaccgaca acgccaagac catcatcgtg 660
cagctgaagg agagcgtgga gatcaactgc acccgcccca acaacaacac ccgcaagagc 720
atcaccatcg geoeggeeg egeettetae gecaceggeg acateategg egacateege 780
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<212> DNA
<213> Artificial Sequence
<220>
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cccgtgtgga aggaggccac caccacctg ttctgcgcca gcgacgccaa ggcctacgac 180
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gagatcgtgc tggagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 300
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 360
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	gcaacatcag					
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